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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:47:02 ; Search time 2534.83 Seconds
(without alignments)
1166.064 Million cell updates/sec

Title: US-10-624-932C-2_COPY_163_223

Perfect score: 326
Sequence: 1 EQGIVLPCRPPEGIPPAEVE.....HSLVVROARLADTANYTCVA 61

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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9: gb.pr.*
10: gb.rc.*
11: gb.sts.*
12: gb.sv.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	326	100.0	2230	6	CQ845766 Sequence
2	326	100.0	2230	9	AK131380 Homo sapi
3	326	100.0	2697	6	AX268596 Sequence
4	326	100.0	2697	6	AX451652 Sequence

5	326	100.0	2697	10	RNU87305	U87305 Rattus norv
6	326	100.0	2752	6	CQ449572	AX449572 Sequence
7	326	100.0	2784	6	CQ730306	CQ730306 Sequence
8	326	100.0	2881	6	AX527916	AX527916 Sequence
9	326	100.0	3014	6	BD057524	BD057524 Netrin re
10	326	100.0	3580	6	AX367094	AX367094 Sequence
11	326	100.0	3992	10	MMU487852	AJ487852 Mus muscu
12	326	100.0	4294	10	AK122575	AK122575 Mus muscu
13	321	98.5	3944	10	BC058084	BC058084 Mus muscu
14	295	90.5	171419	2	AC135142	AC135142 Rattus no
15	270.5	83.0	121282	9	AC027318	AC027318 Homo sapi
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17	270.5	83.0	168168	2	AC012283	AC012283 Homo sapi
18	267	81.9	242128	2	AC123700	AC123700 Mus muscu
19	245	75.2	1482	5	AY764374	AY764374 Danio rer
20	245	75.2	9299	10	MMU72634	U72634 Mus musculu
21	242	74.2	2612	6	CQ881064	CQ881064 Sequence
22	242	74.2	2780	6	CQ881054	CQ881054 Sequence
23	242	74.2	2986	6	CQ881052	CQ881052 Sequence
24	242	74.2	3646	6	CQ881060	CQ881060 Sequence
25	242	74.2	3646	9	AF055634	AF055634 Homo sapi
26	242	74.2	9328	10	AB118026	AB118026 Rattus no
27	237	72.7	2962	5	AY187310	AY187310 Gallus ga
28	236	72.4	2270	9	BC041156	BC041156 Homo sapi
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32	230	70.6	2838	10	RNU87306	U87306 Rattus norv
33	230	70.6	2860	6	AX686445	AX686445 Sequence
34	230	70.6	2860	6	AX686447	AX686447 Sequence
35	230	70.6	2895	6	AX512281	AX512281 Sequence
36	230	70.6	2995	6	AX497288	AX497288 Sequence
37	230	70.6	3672	10	BC048162	BC048162 Mus muscu
38	230	70.6	3672	10	BC057560	BC057560 Mus muscu
39	230	70.6	3770	9	AY126437	AY126437 Homo sapi
40	230	70.6	3788	10	MMU487853	AJ487853 Mus muscu
41	230	70.6	3884	6	AR528525	AR528525 Sequence
42	230	70.6	3884	6	AX464012	AX464012 Sequence
43	230	70.6	3884	9	AX358351	AX358351 Homo sapi
44	230	70.6	3933	6	CQ850929	CQ850929 Sequence
45	230	70.6	3933	9	AK128132	AK128132 Homo sapi

ALIGNMENTS

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CQ845766	Sequence	4413 from Patent EP1440981.			
LOCUS	CQ845766				
DEFINITION	CQ845766				
ACCESSION	CQ845766				
VERSION	CQ845766.1	GI:50895365			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE					
AUTHORS	Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J., Isono,Y., Nagai,K. and Irie,R.				
TITLE	Full-length human cdna				
JOURNAL	Patent: EP 1440981-A 4413 28-JUL-2004;				
FEATURES	Research Association for Biotechnology (JP)				
source	Location/Qualifiers				
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		Matches: 61
		Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

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QY 1 GluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGlu 20
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 QY 21 TrrLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
 DB 616 TGGCTCCGACGACGAGGACTGGTGGACCGTCCCTGGACCCCAATGTATACATCACGGGG 675
 QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
 DB 676 GAGCACAGCCTGGTGGTGGACGAGCGCGCTTGTGTACAGCGGCCCACTACACCTGCCTG 735
 QY 61 Ala 61
 DB 736 GCC 738

RESULT 2
 AKI31380 2230 bp mRNA linear PRI 07-MAY-2004
 LOCUS Homo sapiens cDNA FLJ16449 fis, clone BRAWH2006395, highly similar
 DEFINITION to Rattus norvegicus transmembrane receptor Unc5H1.
 ACCESSION AKI31380
 VERSION AKI31380.1 GI:47077220
 KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Tanigami,A., Fujiwara,T., Shibahara,T., Goto,Y., Hirao,M.,
 Shimizu,F., Wakebe,H., Ono,T., Hishigaki,H., Watanabe,T., Ozaki,K.,
 Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A.,
 Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K.,
 Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y.,
 Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K.,
 Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A.,
 Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masubo,Y., Nagai,K.
 and Isogai,T.
 NEBO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 2230)
 Isogai,T. and Yamamoto,J.
 Direct Submission

TITLE Submitted (01-MAR-2004) Takao Isogai, FLJ Project (HRI Team); 2-6-7
 JOURNAL Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
 AUTHORS Isogai,T. and Yamamoto,J.
 TITLE Direct Submission
 JOURNAL Submitted (01-MAR-2004) Takao Isogai, FLJ Project (HRI Team); 2-6-7
 COMMENT (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 NEBO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
 HRI, and Biotechnology Center, National Institute of Technology and
 Evaluation; clone selection for full insert sequencing: HRI and
 RAB; annotation: HRI and RAB.

FEATURES
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 SLEQIVLPCRPPEGIPPAEVEWLRNEDLDVPSLDPNVYITREHSLVVRQARLADTAN
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ORIGIN

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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x AKI31380 (1-2230)

QY 1 GluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGlu 20
 DB 556 GAGCAGGCGCATCGTCTGCCCTGCCCTCCACCGGAGGCGCATCCCTCCAGCGGAGTGGAG 615
 QY 21 TrrLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
 DB 616 TGGCTCCGACGACGAGGACTGGTGGACCGTCCCTGGACCCCAATGTATACATCACGGGG 675
 QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
 DB 676 GAGCACAGCCTGGTGGTGGACGAGCGCGCTTGTGTACAGCGGCCCACTACACCTGCCTG 735
 QY 61 Ala 61
 DB 736 GCC 738

RESULT 3
 AX268596 2697 bp DNA linear PAT 29-OCT-2001
 LOCUS AX268596 Sequence 15 from Patent WO01/5440.
 DEFINITION AX268596
 ACCESSION AX268596
 VERSION AX268596.1 GI:16541710
 KEYWORDS Rattus sp.
 SOURCE Rattus sp.
 ORGANISM Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE
 1 Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and
 Pratt,J.Y.

AUTHORS Schizophrenia related genes
 TITLE Patent: WO 01/5440-A 15 11-OCT-2001;
 JOURNAL WELFIDE CORPORATION (JP)
 LOCATION/Qualifiers

FEATURES
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 1..2697
 /organism="Rattus sp."
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ORIGIN

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 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

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QY 1 GluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGlu 20
 DB 487 GAGCAAGGCATTGTACTACCTTGTGCGCCCCCAGAAAGGAATCCCCCAGCTGAGGTGGAG 546

Rattus.
1 (bases 1 to 2697)
Leonardo,E.D., HincK,L., Masu,M., Keino-Masu,K., Ackerman,S.L. and
Tessier-Lavigne,M.
Vertebrate homologues of C. elegans UNC-5 are candidate netrin
receptors
NATURE 386 (6627), 833-838 (1997)
97271897
9126742
2 (bases 1 to 2697)
Leonardo,E.D., HincK,L., Masu,M., Keino-Masu,K. and
Tessier-Lavigne,M.
Direct Submission
Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus, San
Francisco, CA 94143-0452, USA
Location/Qualifiers
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/dev_stage="18 day embryo and 13 day embryo"
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/protein_id="AAB57678.1"
/db_xref="GI:2055392"
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SLQGLVLCPRPEGIPAEVZLNEDLVDSLPDNPVITREHSLVYQARLADTAN
YTCVAKNIVARRRSTAAVIVYNGWSTWSEVSCSACGRGWKRSCTNPAPLN
GAFCEGQNVQATACILCPDVGSSWSKNSACGLDTHWRSRECSDPAPRKGEGEC
RGADLTNRCTSDLCHTASCEVDALYIGLVAVAVCLFLLALLGLIYCRKEGLDS
DVADSSILTSPGQPVSIKPSKADNPHLITIQDLSLTITTYOGLSCRODGPSPKFLQ
SNGHLSILPDSGRHTLHSSPTSEADSFVSRILSTONYFRSLPRGTSNMAVGTNFKLG
RLMIPNTGISLLIPDAIPRKIYEIYLTLPKEDVRLPLAGCQTLLSPVSCGPPGV
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QLEKLGGLGIQEPRLVHPKDSYHNLRLSIHDVPVSLMKSLLVSYQETPFYHWNIGT
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ORIGIN

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Score: 326.00 Matches: 61
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Query Match: 100.00% Indels: 0
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Qy 1 GluInGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGlu 20
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Db 547 TGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATCAGCGCG 606
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 607 GAGCAGAGCTTAGTCTGTGGTTCAGGCCCGCCCTGGCCGACACGGCCAACTACACCTGTGTG 666
Qy 61 Ala 61
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Db 667 GCC 669

RESULT 6
AX449572

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LOCUS      AX449572      2752 bp      DNA      linear      PAT 03-JUL-2002
DEFINITION Sequence 1 from Patent WO0210216.
ACCESSION  AX449572
VERSION    AX449572.1  GI:21698195
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Padigaru,M., Mezes,P., Mishra,V., Burgess,C., Casman,S.,
            Grosse,W.M., Alsbrook,J.P., Lepley,D.M., Gerlach,V.L.,
            Macdonald,J.R. and Smithson,G.
TITLE     Proteins and nucleic acids encoding same
JOURNAL   Patent: WO 0210216-A 1 07-FEB-2002;
            Curagen Corporation (US)
FEATURES   source
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            /mol_type="unassigned DNA"
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Qy 21 TrpLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIleThrArg 40
Db 592 TGGCTCCCGAAGCAGGAGACTGGTGACCGCGCTCCCTGGACCCCAATGTATATACATCACGCGG 651
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 652 GAGCACACCTGGTGTGGACAGCGCCGCTTGCTGACACGGCCAACTACACCTCGGTG 711
Qy 61 Ala 61
Db 712 GCC 714
RESULT 7
LOCUS      CQ730306      2784 bp      DNA      linear      PAT 03-FEB-2004
DEFINITION Sequence 16240 from Patent WO02068579.
ACCESSION  CQ730306
VERSION    CQ730306.1  GI:42303801
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
JOURNAL   Patent: WO 02068579-A 16240 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES   Location/Qualifiers
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Db 487 GAGCAGGCGATCGTCTGCCCTCCCGTCCACCGGAGGCATCCCTCCAGCGAGGTGGAG 546
Qy 21 TrpLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIleThrArg 40
Db 547 TGGCTCCCGAAGCAGGAGACTGGTGACCGCGCTCCCTGGACCCCAATGTATATACATCACGCGG 606
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 607 GAGCACAGCCTGGTGTGGTGGACAGCGCCGCTTGCTGACACGGCCAACTACACCTCGGTG 666
Qy 61 Ala 61
Db 667 GCC 669
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DEFINITION Sequence 1 from Patent WO0229038.
ACCESSION  AX527916
VERSION    AX527916.1  GI:25172359
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Herrmann,J.L., Rastelli,L. and Shinkets,R.A.
TITLE     Novel proteins and nucleic acids encoding same and antibodies
            directed against these proteins
            Patent: WO 0229038-A 1 11-APR-2002;
            Curagen Corporation (US)
FEATURES   Location/Qualifiers
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Query Match:    100.00%      Indels:      0
DB:             6      Gaps:      0
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Db 633 TGGCTCCCGAAGCAGGAGACTGGTGACCGCGCTCCCTGGACCCCAATGTATATACATCACGCGG 692
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 693 GAGCACAGCCTGGTGTGGTGGACAGCGCCGCTTGCTGACACGGCCAACTACACCTCGGTG 752
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Qy      61 Ala 61
Db      753 GCC 755

RESULT 9
BD057524
LOCUS   BD057524
DEFINITION Netrin receptors.
ACCESSION BD057524
VERSION   BD057524.1 GI:22603130
KEYWORDS JP 2001505062-A/1.
SOURCE   synthetic construct
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3014)
AUTHORS Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.
TITLE    Netrin receptors
JOURNAL  Patent: JP 2001505062-A 1 17-APR-2001;
          THE REGENTS OF THE UNIV OF CALIFORNIA
COMMENT  PN JP 2001505062-A/1
          PD 17-APR-2001
          PF 19-FEB-1998 JP 1998536840
          PR 19-FEB-1997 US 08/808982
          PI MARC TESSIER LAVIGNE, DAVID E LEONARDO, LINDSAY HINCK, MASAYUKI
          PI MASU,
          PI KAZUKO KEINO MASU
          PC C07K1/00, C07K14/00, C07K17/00, C07H21/02, C07H21/04, G01N33/53 CC
          Strandedness: Double;
          CC Topology: Linear;
          FH Key Location/Qualifiers.

FEATURES
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Score:          326.00      Matches:      61
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             6           Gaps:          0

US-10-624-932C-2_COPY_163_223 (1-61) x BD057524 (1-3014)

Qy      1 GluGlnGlyIleValLeuProCybArgProProGluGlyIleProProAlaGluValGlu 20
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Qy      21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
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Qy      41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db      607 GAGCACAGCCTAGTGTGCGTCAGCGCGCTGGCGGACACGGCCAACTACACCTGTGTG 666

Qy      61 Ala 61
Db      667 GCC 669

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LOCUS   AX367094
DEFINITION Sequence 13 from Patent WO0198354.
ACCESSION AX367094
VERSION   AX367094.1 GI:18855296
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Griffin,J.A., Kallick,D.A., Tribouley,C.M., Yue,H., Nguyen,D.B.,
Tang,Y.T., Lal,P., Policky,J.L., Azimzai,Y., Lu,D.A., Graul,R.,
Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O.,
Patterson,C., Yang,J., Xu,Y., Warren,B.A., Ding,L. and
Sanjanwala,M.S.
Receptors
Patent: WO 0198354-A 13 27-DEC-2001;
Incyte Genomics, Inc. (US)
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US-10-624-932C-2_COPY_163_223 (1-61) x AX367094 (1-3580)

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Qy      41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
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Qy      61 Ala 61
Db      670 GCC 672

RESULT 11
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LOCUS   MMU487852
DEFINITION Mus musculus mRNA for netrin receptor Unc5h1 (Unc5h1 gene).
ACCESSION AJ487852
VERSION   AJ487852.1 GI:22035783
KEYWORDS netrin receptor Unc5h1; Unc5h1 gene.
SOURCE   Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1
Engelkamp,D.
Cloning of three mouse Unc5 genes and their expression patterns at
mid-gestation
Mech. Dev. 118 (1-2), 191-197 (2002)
MEDLINE 22239710
PUBMED 12351186
REFERENCE 2 (bases 1 to 3992)
AUTHORS Engelkamp,D.
TITLE    Direct Submission
JOURNAL  Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for
          Brain Research, Deutschordenstrasse 46, Frankfurt 60528, GERMANY
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	/protein_id="CAD32250.1"		(E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)	
	/db_xref="GI:22035784"		The CREATE program supported by Japan science and technology	
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			VERSION	
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			AUTHORS	
			TITLE	
			JOURNAL	
			REFERENCE	
			2 (bases 1 to 4294)	
			Mus musculus (house mouse)	
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
			Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
			1	
			Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Aizawa,H., Yuasa,S.,	
			Nakajima,D., Nagase,T., Ohara,O. and Koga,H.	
			Prediction of the coding sequences of mouse homologues of KIAA	
			gene: II. The complete nucleotide sequences of 400 mouse	
			KIAA-homologous cDNAs identified by screening of terminal sequences	
			of cDNA clones randomly sampled from size-fractionated libraries	
			DNA Res. 10, 35-48 (2003)	
			2 (bases 1 to 4294)	
			Mus musculus (house mouse)	
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
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			Prediction of the coding sequences of mouse homologues of KIAA	
			gene: II. The complete nucleotide sequences of 400 mouse	
			KIAA-homologous cDNAs identified by screening of terminal sequences	
			of cDNA clones randomly sampled from size-fractionated libraries	
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			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
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			Prediction of the coding sequences of mouse homologues of KIAA	
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			of cDNA clones randomly sampled from size-fractionated libraries	
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			2 (bases 1 to 4294)	
			Mus musculus (house mouse)	
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
			Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
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			Prediction of the coding sequences of mouse homologues of KIAA	
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ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 3844)

REFERENCE
AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Frange, C., Rana, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullighy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skaleka, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 3844)

REFERENCE
AUTHORS
JOURNAL

Strausberg, R.
Direct Submission
Submitted (08-SEP-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library Preparation: M. Bento Soares, University of Iowa

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Boedet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letitia Hsiao, Martin Krzywinski, Reta Kuteche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Teai, Natassja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAP Plate: 126 Row: b Column: 11

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 23346570.

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Some (but not all) of these domains form homotypic and
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ORIGIN

Alignment Scores:

Pred. No.:	9,7e-29	Length:	3844
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Percent Similarity:	98.36%	Conservative:	0
Best Local Similarity:	98.36%	Mismatches:	1
Query Match:	98.47%	Indels:	0
DB:	10	Gaps:	0

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Qy	41	GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyThrCysVal	60
Db	858	GAGCACACCTTAGTGTGCGGACGCCCGCTCCGACACTCCCACTACACTCTCGGTG	917
Qy	61	Ala 61	
Db	918	GCC 920	

RESULT 14

AC135142/c

LOCUS	AC135142	171419 bp	DNA	linear	HTG 15-NOV-2002																								
DEFINITION	Rattus norvegicus clone CH230-169P5, *** SEQUENCING IN PROGRESS																												
ACCESSION	AC135142																												
VERSION	AC135142.2 GI:25007239																												
KEYWORDS	HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.																												
SOURCE	Rattus norvegicus (Norway rat)																												
ORGANISM	Rattus norvegicus																												
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.																												
REFERENCE	1 (bases 1 to 171419)																												
AUTHORS	Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovac, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuewa, L., Loulsegred, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, W., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwakoleme, O., Okwuonu, G., Olarnpusagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfamkoch, C., Plopper, F., Poin Dexter, A., Popovic, D., Primus, E., Pu, L., Pu, L., Pu, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shateman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C. D., Smajls, D., Sneed, A., Sodergren, E., Song, X. Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasan, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.																												
	Direct Submission																												
JOURNAL	Unpublished																												
REFERENCE	2 (bases 1 to 171419)																												
AUTHORS	Rat Genome Sequencing Consortium.																												
TITLE	Direct Submission																												
JOURNAL	Submitted (08-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA																												
REFERENCE	3 (bases 1 to 171419)																												
AUTHORS	Rat Genome Sequencing Consortium.																												
TITLE	Direct Submission																												
JOURNAL	Submitted (15-NOV-2002) Human Genome Sequencing Center, Department																												
COMMENT	<p>of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA</p> <p>On Nov 15, 2002 this sequence version replaced gi:23578050. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.</p> <p>----- Genome Center Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu</p> <p>----- Project Information Center project name: KCMS Center clone name: CH230-169P5 ----- Summary Statistics Assembly program: Phrap; version 0.990329 Consensus quality: 127081 bases at least Q40 Consensus quality: 131254 bases at least Q30 Consensus quality: 133849 bases at least Q20 Estimated insert size: 128800; sum-of-contigs estimation Quality coverage: 5x in Q20 bases; sum-of-contigs estimation</p> <p>----- * NOTE: Estimated insert size may differ from sequence length * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). * NOTE: This is a 'working draft' sequence. It currently * consists of 9 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.</p> <p>1 18754: contig of 18754 bp in length 18755: gap of unknown length 18855: contig of 129006 bp in length 147861: gap of unknown length 147960: gap of unknown length 159835: contig of 11875 bp in length 159936: gap of unknown length 161085: contig of 1150 bp in length 161086: gap of unknown length 161186: contig of 1304 bp in length 162489: contig of 1459 bp in length 162589: gap of unknown length 164048: contig of 1459 bp in length 164049: gap of unknown length 165318: contig of 1170 bp in length 165319: gap of unknown length 165418: contig of 2149 bp in length 165419: gap of unknown length 167567: gap of unknown length 171419: contig of 3752 bp in length.</p> <p>FEATURES source 1..171419 /organism="Rattus norvegicus" /mol_type="genomic DNA" /db_xref="taxon:10116" /clone="CH230-169P5"</p>																												
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Pred. No.:	4.45e-24	Length:	171419																										
Score:	295.00	Matches:	61																										
Percent Similarity:	59.22%	Conservative:	0																										
Best Local Similarity:	59.22%	Mismatches:	0																										
Query Match:	90.49%	Indels:	42																										
DB:	2	Gaps:	1																										

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Qy 18 ----- 18
Db 27205 AGGGGTACCGGTGCCAGACCTCTGCTCTACCTAAAGCTCAGACTCTCTGGCTTCCCC 27146
Qy 18 ----- 18
Db 27145 TCCCCAGTCTCACTCTGTACCTGTGTCAGGCAGCATGGGTCTTCTCCCTAG 27086
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Db 27085 GTGGAGTGGCTTCGAATAGAGACTCTGTGGACCCCTCCCTCGATCCCATGTGTACATC 27026
Qy 39 ThrArgGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 58
Db 27025 ACGCGGGAGCACAGCTAGTGTGCTGTCAGGCCCGCTGGCGGACACGCGCAACTACACC 26966
Qy 59 CysValAla 61
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VERSION HTG
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 121282)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 121282)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 121282)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 121282)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Dec 1, 2002 this sequence version replaced gi:19224786.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1
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FEATURES
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Score: 270.50 Matches: 60
Percent Similarity: 59.41% Conservative: 0
Best Local Similarity: 59.41% Mismatches: 1
Query Match: 82.98% Indels: 41
DB: 9 Gaps: 1
US-10-624-932C-2_COPY_163_223 (1-61) x AC027318 (1-121282)
Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluVal--- 19
Db 11386 GAGCAGGCAATTGTACTACCTTGTGCCCCCAGAGGAATCCCCCAGCTGAGGTGAGT 11444
Qy 19 ----- 19
Db 11445 GGCTCCTCTAGTGGCCAGCTCTGGACCTGGGCTCTGCTGGTACACCTGGCAGGGGCA 11504
Qy 20 -----Glu 20
Db 11505 CTCTGGGCAGGCCAGCATGGCTGGCAGTACATGGCAGGGCTCCCTCCCTAGGTGGAG 11564
Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 11565 TGGCTCCGGAAACGAGGACCTGTGGTGGACCCCTCCCTGGACCCCAATGTATACATCACGGG 11624
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 11625 GAGCAGACCTGTGTGGTGGCAGCGCCGCTTGTCTGACACGGCCACTACACCTGCGGTG 11684
Qy 61 Ala 61
Db 11685 GCC 11687

Search completed: September 9, 2005, 09:39:41
Job time : 2571.83 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 20:54:46 ; Search time 315.473 Seconds
(without alignments)
1144.643 Million cell updates/sec

Title: US-10-624-932C-2_COPY_163_223

Perfect score: 326
Sequence: 1 EQGIVLPCRPPGPIPAEVE.....HSLVVRQARLADTANYTCVA 61

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	326	100.0	2463	12 ADH71623	Adh71623 Human gen
7	326	100.0	2575	12 ADH71621	Adh71621 Human gen
8	326	100.0	2697	6 AAS16843	Aas16843 Rat netri
9	326	100.0	2697	6 ABK52891	Abk52891 Human net
10	326	100.0	2752	6 ABK37922	Abk37922 cDNA enco
11	326	100.0	2752	12 ADH71617	Adh71617 Human gen
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19	326	100.0	2881	12 ADH71609	Adh71609 Human gen
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28	326	100.0	2907	4 AAK52261	Aak52261 Human pol
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30	326	100.0	3561	12 ADL06497	Adl06497 Human tum
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33	242	74.2	2780	13 ADR99251	Adr99251 Human sRO
34	242	74.2	2796	10 AAL56266	Aal56266 Human thr
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38	230	70.6	2831	2 AAV52942	Avs52942 Rat UNC-5
39	230	70.6	2838	12 ADO09501	Ado09501 Rat ttrans
40	230	70.6	2860	6 ABT06279	Abt06279 Human NOV
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44	230	70.6	3501	11 ADN39805	Adn39805 Cancer/an
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ALIGNMENTS

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AC ADH71611;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21b SEQ ID NO:507.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.

XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX Homo sapiens.

XX WO2003102155-A2.

XX 11-DEC-2003.

XX 03-JUN-2003; 2003WO-US017430.

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XX 14-JUN-2002; 2002US-0389118P.

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XX 17-JUN-2002; 2002US-0389729P.

XX 17-JUN-2002; 2002US-0389742P.

XX 18-JUN-2002; 2002US-0389848P.

XX 19-JUN-2002; 2002US-0390068P.

XX 19-JUN-2002; 2002US-0390209P.

XX 21-JUN-2002; 2002US-0390763P.

XX 17-JUL-2002; 2002US-0396706P.

XX 06-AUG-2002; 2002US-0401628P.

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XX 13-AUG-2002; 2002US-0406317P.

XX 15-AUG-2002; 2002US-0403617P.

XX 26-AUG-2002; 2002US-0406182P.

PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
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PR 09-OCT-2002; 2002US-0417186P.
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PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

XX (CURA-) CURAGEN CORP.

XX Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;

XX WPI; 2004-081935/08.

XX P-PSDB; ADH71620.

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT creating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 21; SEQ ID NO 515; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A

CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaeamic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

XX Sequence 1002 BP; 193 A; 311 C; 335 G; 163 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	9.76e-35	Length:	1002
Score:	326.00	Matches:	61
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-624-932C-2_COPY_163_223 (1-61) x ADH71619 (1-1002)

Oy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProGluValGlu 20

DB 418 GAGCAGGGCATCGTGGCTGCCCTCCACCGAGGGCATCCCTCCAGCGAGGTGGAG 477

Oy 21 TriLeuArgAenGluAspLeuValAspProSerLeuAspProAenValThrArg 40

```
Db 478 TGCTCGGACGAGGACCTGGTGGACCCCTCCCTGGACCCCAATGTATACATCACGGG 537
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaIenTyrThrCysVal 60
Db 538 GAGCAGACGCTGGTGGTGGCGACAGGCGCGCTTGCTGACACGGCCAACTACACCTGGTG 597
Qy 61 Ala 61
Db 598 GCC 600

RESULT 3
ADH71615
ID ADH71615 standard; DNA; 1009 BP.
XX AC ADH71615;
XX DT 25-MAR-2004 (first entry)
XX DE Human gene of the invention NOV21d SEQ ID NO:511.
XX KW db; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX OS Homo sapiens.
XX PN WC2003102155-A2.
XX PD 11-DEC-2003.
XX PF 03-JUN-2003; 2003WO-US017430.
XX 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386047P.
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PR 08-JUN-2002; 2002US-0386453P.
PR 09-JUN-2002; 2002US-0386854P.
PR 10-JUN-2002; 2002US-0386916P.
PR 11-JUN-2002; 2002US-0386971P.
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PR 15-JUN-2002; 2002US-0387400P.
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PR 02-OCT-2002; 2002US-0389884P.
PR 03-OCT-2002; 2002US-0389884P.
PR 04-OCT-2002; 2002US-0389884P.
PR 05-OCT-2002; 2002US-0389884P.
PR 06-OCT-2002; 2002US-0389884P.
PR 07-OCT-2002; 2002US-0389884P.
PR 08-OCT-2002; 2002US-0389884P.
PR 09-OCT-2002; 2002US-0389884P.
PR 10-OCT-2002; 2002US-0389884P.
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PR 12-OCT-2002; 2002US-0389884P.
PR 13-OCT-2002; 2002US-0389884P.
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PR 16-OCT-2002; 2002US-0389884P.
PR 17-OCT-2002; 2002US-0389884P.
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PR 28-OCT-2002; 2002US-0389884P.
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PR 02-NOV-2002; 2002US-0389884P.
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PR 04-NOV-2002; 2002US-0389884P.
PR 05-NOV-2002; 2002US-0389884P.
PR 06-NOV-2002; 2002US-0389884P.
PR 07-NOV-2002; 2002US-0389884P.
PR 08-NOV-2002; 2002US-0389884P.
PR 09-NOV-2002; 2002US-0389884P.
PR 10-NOV-2002; 2002US-0389884P.
PR 11-NOV-2002; 2002US-0389884P.
PR 12-NOV-2002; 2002US-0389884P.
XX (CURA-) CURAGEN CORP.
XX PA Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
XX Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
XX Bittenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
XX Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
XX MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS, Rastelli L;
XX Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
XX Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
XX Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
XX Zhong H;
XX WFI; 2004-081935/08.
XX P-PSDB; ADH71616.
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
XX treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
XX obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX Example 21; SEQ ID NO 511; 1880pp; English.
XX The invention relates to a novel isolated polypeptide (NOVX). A
XX polypeptide of the invention has cytostatic, immunomodulator,
XX neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
XX antilipaemic activity, and may have a use in gene therapy, and as a
XX vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
XX any of the 303 fully defined nucleotide sequences given in the
XX specification. The polypeptide is useful in the manufacture of a
XX medicament for treating a syndrome associated with a human disease. The
XX polypeptide, polynucleotide and antibody are useful in diagnosing,
XX treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
XX Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
XX diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
XX further used as hybridisation probes, in chromosome mapping, tissue
```

PR 11-JUN-2002; 200205-0387610P.

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 509; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaeamic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 1009 BP; 195 A; 314 C; 336 G; 164 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.85e-35 Length: 1009
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932c-2_COPY_163_223 (1-61) x ADH71613 (1-1009)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Db 422 GAGCAGGGCATCGTGTGCTGCCCTCCACCGGAGGGCATCCCTCCAGCGAGGTGGAG 481

Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProLeuValTyrIleThrArg 40
Db 482 TGGCTCCGGAACGAGGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATACATCAGCGG 541

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaIleThrCysVal 60
Db 542 GAGCAGACGCTGGTGGTGGCAGAGCGCCGCTTGTCTGACACGCCCACTACCTCGGTG 601

Qy 61 Ala 61
Db 602 GCC 604

RESULT 5
ADQ67252
ID ADQ67252 standard; cDNA; 2230 BP.
XX
XX AC ADQ67252;
XX
XX DT 07-OCT-2004 (first entry)
XX
XX DE Novel human cDNA sequence #2225.
XX
XX SS; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KW cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW cancer.
XX
XX OS Homo sapiens.
XX
XX PN EP1440981-A2.
XX
XX PD 28-JUL-2004.
XX
XX PF 21-JAN-2004; 2004EP-00001196.

XX 21-JAN-2003; 2003JP-00102206.
PR 09-MAY-2003; 2003JP-00131392.
XX
XX (SEAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Nagai K, Irie R;
XX WPI; 2004-535376/52.
DR P-PSDB; ADQ67559.
XX
XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
XX Claim 1; SEQ ID NO 4413; 2449pp; English.
XX
XX The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a nucleotide
CC sequence of the invention.
XX
SQ Sequence 2230 BP; 458 A; 947 C; 462 G; 363 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.78e-34 Length: 2230
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932c-2_COPY_163_223 (1-61) x ADQ67252 (1-2230)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Db 556 GAGCAGGGCATCGTGTGCTGCCCTCCACCGGAGGGCATCCCTCCAGCGAGGTGGAG 615

Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProLeuValTyrIleThrArg 40
Db 616 TGGCTCCGGAACGAGGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATACATCAGCGG 675

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaIleThrCysVal 60
Db 676 GAGCAGACGCTGGTGGTGGCAGAGCGCCGCTTGTCTGACACGCCCACTACCTCGGTG 735

Qy 61 Ala 61
Db 736 GCC 738

RESULT 6
ADH71623
ID ADH71623 standard; DNA; 2463 BP.
XX
XX AC ADH71623;
XX
XX DT 25-MAR-2004 (first entry)
XX
XX DE Human gene of the invention NOV21h SEQ ID NO:519.
XX
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
XX OS Homo sapiens.
XX

Db 598 GCC 600
RESULT 7
ADH71621
ID ADH71621 standard; DNA; 2575 BP.
XX AC ADH71621;
XX AC
XX 25-MAR-2004 (first entry)
XX DE Human gene of the invention NOV21g SEQ ID NO:517.
XX KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX OS Homo sapiens.
XX PN W02003102155-A2.
XX PD 11-DEC-2003.
XX PF 03-JUN-2003; 2003WO-US017430.
XX PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
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PR 11-JUN-2002; 2002US-0387702P.
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PR 12-JUN-2002; 2002US-0388022P.
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PR 13-JUN-2002; 2002US-0389123P.
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PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX PA (CURA-) CURAGEN CORP.
XX PI Alsbrook JP, Alvarez E, Anderson DW, Boldog PL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Etenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg MB, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71622.
DR XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 517; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaeamic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2575 BP; 490 A; 873 C; 754 G; 458 T; 0 U; 0 Other;
Alignment Scores: 3.35e-34 Length: 2575
Pred. No.: 326.00 Matches: 61
Score: 100.00% Conservative: 0
Percent Similarity:

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x ADH71621 (1-2575)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
 Db 462 GAGCAGGCGCATCGTGCCTGCCCTCCACCGGAGGCATCCCTCCAGCGAGGTGGAG 521

Qy 21 TrpLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIleThrArg 40
 Db 522 TGGCTCCGGACGAGGACCTGGTGACCCGCTCCGACCCCAATGTATATACATCACGCGG 581

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAenTyrThrCysVal 60
 Db 582 GAGCAGCGCTGGTGGTGACAGCGCCGCTTCTGACAGCGCCCACTACACCTGGGTG 641

Qy 61 Ala 61
 Db 642 GCC 644

RESULT 8
 AAS16843
 ID AAS16843 standard; cDNA; 2697 BP.
 AC AAS16843;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Rat netrin receptor UNC5H1 (YSG7) cDNA.
 XX
 XX YSG7; schizophrenia; chronic animal model; LCGU; netrin receptor;
 KW local cerebral glucose utilisation; phosphodiesterase 1-alpha; UNC5H1;
 KW calcium-independent alpha-latrotoxin receptor; CIRL; trkB; synapsin 1A;
 KW epithelial discoidin domain receptor 1; synapsin 1B; neuroleptic; ss;
 KW tumour necrosis factor alpha; TNF-alpha; rat.
 XX
 OS Rattus sp.
 XX
 PH Key Location/Qualifiers
 FT CDS 1..2697
 FT /*tag= a
 FT /product= "Rat netrin receptor UNC5H1"
 XX
 XX WO200175440-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 02-APR-2001; 2001WO-GB001486.
 XX
 XX 31-MAR-2000; 2000GB-00007880.
 PR
 PR 26-MAY-2000; 2000GB-00012768.
 XX
 PA (WELF-) WELFIDE CORP.
 XX
 XX Cochran S, Paterson G, Ohashi Y, Morris B, Pratt J;
 PI
 XX WPI; 2002-010813/01.
 DR
 DR P-PSDB; AAU10543.
 XX
 XX Novel chronic animal model of schizophrenia, useful for identifying anti-
 PT psychotic drugs and genes that are associated with schizophrenia.
 PR
 XX Claim 1; Fig 8a; 79pp; English.
 PS
 XX The invention relates to YSG polynucleotide fragments for use in
 CC diagnosing and/or developing treatments for schizophrenia using chronic
 CC animal models. The polynucleotides and their encoded polypeptides are
 CC used for identification of compounds which modulate the expression of YSG
 CC molecules, leading to the manufacture of schizophrenia medications. The
 CC sequences can also be used for testing candidate compounds for any effect
 CC on the polypeptides. Anti-schizophrenic effects of a compound can be

determined by measuring local cerebral glucose utilisation (LCGU) or
 comparing its expression level with that of a control group. The
 sequences are useful in the identification of genes associated with
 schizophrenia states and in the development of an antibody. The sequences
 of the invention include phosphodiesterase 1-alpha, calcium-independent
 alpha-latrotoxin receptors (CIRL)-1,2k3, epithelial discoidin domain
 receptor 1 (trkB), netrin receptor (UNC5H1), synapsins 1A and 1B and
 tumour necrosis factor (TNF) alpha. This sequence represents rat netrin
 receptor UNC5H1 (YSG7) DNA

XX
 SQ Sequence 2697 BP; 541 A; 864 C; 766 G; 526 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3.56e-34 Length: 2697
 Score: 326.00 Matches: 61
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x AAS16843 (1-2697)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
 Db 487 GAGCAGGCGCATCGTGCCTGCCCTCCACCGGAGGCATCCCTCCAGCGAGGTGGAG 546

Qy 21 TrpLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIleThrArg 40
 Db 547 TGGCTTCGAAATGAGGACCTGGTGACCCCTCCCTCCGATCCCAATGTATATACATCACGCGG 606

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAenTyrThrCysVal 60
 Db 607 GAGCAGCGCTAGTGCCTGCGTGCAGCGCCGCTCCGACGACGCGCAACTACACCTGTGTG 666

Qy 61 Ala 61
 Db 667 GCC 669

RESULT 9
 ABK52891
 ID ABK52891 standard; DNA; 2697 BP.
 XX
 AC ABK52891;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 XX Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.
 DE
 DE Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human;
 KW neurotropic; neuroprotective; cytoskeletal; antiparkinsonian;
 KW cerebroprotective; cancer; central nervous system; CNS; stroke;
 KW Parkinson's disease; multiple sclerosis; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 1..2697
 FT /*tag= a
 FT /product= "Netrin binding membrane receptor UNC5H-1"
 XX
 XX WO200233080-A2.
 PN
 XX 25-APR-2002.
 XX
 XX 15-OCT-2001; 2001WO-EP011891.
 XX
 XX 16-OCT-2000; 2000US-0240061P.
 PR
 XX (FARB) BAYER AG.
 PA
 XX Koehler RH;
 PI
 XX WPI; 2002-463314/49.
 DR

US-10-624-932c-2_copy_163_223 (1-61) x ABK37922 (1-2752)

Qy 1 GluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGlu 20

Db 532 GAGCAGGGGATCGTCTGCCCTTCCCTCCACGGAGGGATCCCTCCAGCCGAGGTGGAG 591

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTrpIleThrArg 40

Db 592 TGGCTCCGGAACGAGGACCTGGTGGACCGTCCCTGGACCCCAATGTATACATCAGCGG 651

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTrpThrCysVal 60

Db 652 GAGCAGCGCTGGTGGCAGAGCCCGCTTGTGTGACAGCCCAACTACACCTGCGTG 711

Qy 61 Ala 61

Db 712 GCC 714

RESULT 11

ADH71617

ID ADH71617 standard; DNA; 2752 BP.

XX AC ADH71617;

XX DT 25-MAR-2004 (first entry)

XX DE Human gene of the invention NOV21e SEQ ID NO:513.

XX KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;

XX KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;

XX KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;

XX KW obesity; diabetes; infectious disease; metabolic syndrome X;

XX KW dyslipidaemia.

XX OS Homo sapiens.

XX FN WO2003102155-A2.

XX PD 11-DEC-2003.

XX PF 03-JUN-2003; 2003WO-US017430.

XX PR 03-JUN-2002; 2002US-0385120P.

XX PR 04-JUN-2002; 2002US-0385784P.

XX PR 05-JUN-2002; 2002US-0386041P.

XX PR 05-JUN-2002; 2002US-0386047P.

XX PR 06-JUN-2002; 2002US-0386376P.

XX PR 06-JUN-2002; 2002US-0386644P.

XX PR 06-JUN-2002; 2002US-0387016P.

XX PR 07-JUN-2002; 2002US-0387969P.

XX PR 07-JUN-2002; 2002US-0386816P.

XX PR 07-JUN-2002; 2002US-0386931P.

XX PR 07-JUN-2002; 2002US-0386942P.

XX PR 07-JUN-2002; 2002US-0386971P.

XX PR 07-JUN-2002; 2002US-0387262P.

XX PR 08-JUN-2002; 2002US-0296960P.

XX PR 10-JUN-2002; 2002US-0387400P.

XX PR 10-JUN-2002; 2002US-0387535P.

XX PR 11-JUN-2002; 2002US-0387610P.

XX PR 11-JUN-2002; 2002US-0387625P.

XX PR 11-JUN-2002; 2002US-0387634P.

XX PR 11-JUN-2002; 2002US-0387668P.

XX PR 11-JUN-2002; 2002US-0387696P.

XX PR 11-JUN-2002; 2002US-0387702P.

XX PR 11-JUN-2002; 2002US-0387836P.

XX PR 11-JUN-2002; 2002US-0387859P.

XX PR 12-JUN-2002; 2002US-0387933P.

XX PR 12-JUN-2002; 2002US-0387934P.

XX PR 12-JUN-2002; 2002US-0387960P.

XX PR 12-JUN-2002; 2002US-0388022P.

XX PR 12-JUN-2002; 2002US-0388096P.

PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-039006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 15-AUG-2002; 2002US-0406317P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.

PI Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VV, Herrmann JL, Ji W, Kakuda R, Li L, Liu X, Macdougall JR;
PI Maciachian T, Malyankar UM, Mesick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
PI Zhong H;

WPI; 2004-081935/08.

P-PSDB; ADH71618.

New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

Example 21; SEQ ID NO 513; 1880pp; English.

The invention relates to a novel isolated polypeptide (NOVX). A

polypeptide of the invention has cytostatic, immunomodulator,

neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and

antilipemic activity, and may have a use in gene therapy, and as a

vaccine. The polypeptides are encoded by NOVX polynucleotides comprising

CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOX polypeptide of the invention.

SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.66e-34 Length: 2752
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932c-2_copy_163_223 (1-61) x ADH71617 (1-2752)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
|||
Db 532 GAGCAGGCGCATCGTCTGCCCTGCCCTCCACCGGAGGGCATCCCTCCAGCGAGTGGAG 591
|||
Qy 21 TrpLeuArgAenGluAppLeuValAppProSerLeuAppProAenValTyrIleThrArg 40
|||
Db 592 TGGCTCCGGACAGGAGCACCTGGTGGACCCCGTCCCTGGACCCCAATGTATACATCACGCGG 651
|||
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAppThrAlaAenTyrThrCysVal 60
|||
Db 652 GAGCACACGCTGGTGGTGGCAGACGGCCCGCTTGTGACAGCGCCAACTACACCTGGGTG 711
|||
Qy 61 Ala 61
|||
Db 712 GCC 714

RESULT 12
ADH71633
ID ADH71633 standard; DNA; 2880 BP.
AC ADH71633;
XX
DT 25-MAR-2004 (first entry)
XX
XX Human gene of the invention NOV21m SEQ ID NO:529.
XX
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia.
XX
XX Homo sapiens.
XX
XX WO2003102155-A2.
XX
XX 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
XX
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
XX 05-JUN-2002; 2002US-0386047P.
XX 06-JUN-2002; 2002US-0386376P.
XX 06-JUN-2002; 2002US-0386453P.
XX 06-JUN-2002; 2002US-0386864P.
XX 06-JUN-2002; 2002US-0387016P.
XX 07-JUN-2002; 2002US-038796P.
XX 07-JUN-2002; 2002US-0386816P.

PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 08-JUN-2002; 2002US-0387262P.
PR 10-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387658P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0406317P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-041801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.

XX PA
XX PI
PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Etenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;

PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Feyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
XX Zhong H;
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71634.

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
DR treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 21; SEQ ID NO 529; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

XX SQ Sequence 2880 BP; 527 A; 994 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.88e-34 Length: 2880
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x ADH71633 (1-2880)

Qy 1 GluGlnGlyLeuValLeuProCysArgProGluGlyLeuProAlaGluValGlu 20
Db 572 GAGCAGGCGATCGTGTGCTGCGCTCCACCGAGGCGCATCCCTCCAGCGAGGTGGAG 631
Qy 21 TrpLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIleThrArg 40
Db 632 TGGCTCCGGAACGAGGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATACATCACCGCG 691
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAenTyrThrCysVal 60
Db 692 GAGCACAGCCTGGTGGTGGCGACGCGCCGCTTGTCTGACACGGCCAACTACACCTCGGTG 751
Qy 61 Ala 61
Db 752 GCC 754

RESULT 13

ABK49422

ID ABK49422 standard; DNA; 2881 BP.

AC ABK49422;

XX 15-JUL-2002 (first entry)

XX DNA encoding human UNC5-like protein NOV1.

XX Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;
KW cell signal processing; metabolic pathway modulation; cancerous tissue;
KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;
KW chromosome 13; gene; db.

XX Homo sapiens.
OS Key Location/Qualifiers
XX CDS 87..2786
FT /*tag= a
FT /product= "Human UNC5-like protein NOV1"

XX WO200229038-A2.

XX 11-APR-2002.

XX 04-OCT-2001; 2001WO-US031377.

XX 04-OCT-2000; 2000US-0237862P.

XX (CURA-) CURAGEN CORP.

XX Herrmann JL, Rastelli L, Shimkets RA;

XX WPI; 2002-340104/37.

XX P-PSDB; AAU79939.

XX Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for
PT treating cardiomyopathy, atherosclerosis, and cancer.

XX Claim 8; Page 7-8; 180pp; English.

XX The present invention relates to a new NOVX polypeptide having a 900
CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)
CC residue amino acid sequence, as given in the specification. The novel
CC polypeptide, and its encoding polynucleotide, are used to treat
CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell
CC signal processing and metabolic pathway modulation, in a human. Detecting
CC the polypeptide or polynucleotide is useful for identifying cancerous
CC cells. The antibody can be used to treat diabetes or cancer. The host
CC cells can be used to produce non-human transgenic animals useful in drug
CC screening. The present nucleic acid sequence is that of the human UNC5-
CC like NOV1 gene located on chromosome 13. This sequence encodes the human
CC UNC5-like protein NOV1 of the invention

XX SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.88e-34 Length: 2881
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-624-932C-2_COPY_163_223 (1-61) x ABK49422 (1-2881)

Qy 1 GluGlnGlyLeuValLeuProCysArgProGluGlyLeuProAlaGluValGlu 20

Db 573 GAGCAGGCGATCGTGTGCTGCGCTCCACCGAGGCGCATCCCTCCAGCGAGGTGGAG 632

Qy 21 TrpLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIleThrArg 40

Db 633 TGGCTCCGGAACGAGGACCTGGTGGACCCGCTCCCTGGACCCCAATGTATACATCACCGCG 692

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAenTyrThrCysVal 60

Db 693 GAGCACAGCCTGGTGGTGGCGACGCGCCGCTTGTCTGACACGGCCAACTACACCTCGGTG 752

Qy 61 Ala 61

Db 753 GCC 755

RESULT 14

ADG42568

ID ADG42568 standard; cDNA; 2881 BP.

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AC ADG42568;
XX 26-FEB-2004 (first entry)
XX AC
XX ADH71649;
XX AC
XX 25-MAR-2004 (first entry)
XX DE
XX Human gene of the invention NOV21u SEQ ID NO:545.
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia.
XX Homo sapiens.
XX OS
XX WO2003102155-A2.
XX PN
XX 11-DEC-2003.
XX PD
XX PF
XX 03-JUN-2003; 2003WO-US017430.
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
XX 06-JUN-2002; 2002US-0386047P.
XX 06-JUN-2002; 2002US-0386376P.
XX 06-JUN-2002; 2002US-0386453P.
XX 06-JUN-2002; 2002US-0386864P.
XX 06-JUN-2002; 2002US-0387016P.
XX 07-JUN-2002; 2002US-0386796P.
XX 07-JUN-2002; 2002US-0386816P.
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XX 11-JUN-2002; 2002US-0387668P.
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XX 11-JUN-2002; 2002US-0387836P.
XX 12-JUN-2002; 2002US-0387859P.
XX 12-JUN-2002; 2002US-0387933P.
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ID ADH71649 standard; DNA; 2881 BP.
XX AC
XX ADH71649;
XX AC
XX 25-MAR-2004 (first entry)
XX DE
XX Human gene of the invention NOV21u SEQ ID NO:545.
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia.
XX Homo sapiens.
XX OS
XX WO2003102155-A2.
XX PN
XX 11-DEC-2003.
XX PD
XX PF
XX 03-JUN-2003; 2003WO-US017430.
XX 03-JUN-2002; 2002US-0385120P.
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XX 12-AUG-2002; 2002US-0402821P.
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ADG42568;
XX 26-FEB-2004 (first entry)
XX AC
XX ADH71649;
XX AC
XX 25-MAR-2004 (first entry)
XX DE
XX Human gene of the invention NOV21u SEQ ID NO:545.
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia.
XX Homo sapiens.
XX OS
XX WO2003204052-A1.
XX PN
XX 30-OCT-2003.
XX PD
XX PF
XX 04-OCT-2001; 2001US-00970944.
XX 04-OCT-2000; 2000US-0237862P.
XX 04-OCT-2000; 2000US-0237862P.
XX (HERR/) HERRMANN J L.
XX (RAST/) RASTELLI L.
XX (SHIM/) SHIMKETS R A.
XX Herrmann JL, Rastelli L, Shimkets RA;
XX WPI; 2003-900673/82.
XX P-PSDB; ADG42569.
XX New NOVX gene or NOVX-specific antibody, useful for preparing a
XX composition for treating or preventing a NOVX-associated disorder, e.g.,
XX cancer.
XX Claim 9; SEQ ID NO 1; 118pp; English.
XX The invention describes a new isolated polypeptide comprising: a
XX polypeptide or its mature form comprising a sequence not given in the
XX specification; or a variant of (A) where one or more amino acid residues
XX in the variant differs in no more than 15% from the amino acid sequence
XX of the mature form. The pharmaceutical composition may be administered
XX via oral, transdermal, rectal or parenteral route. The polypeptide,
XX nucleic acid or antibody is useful for preparing a composition for
XX treating or preventing a NOVX-associated disorder, e.g., cancer. This
XX sequence encodes a human NOVX protein.
XX SQ Sequence 2881 BP; 526 A; 987 C; 866 G; 502 T; 0 U; 0 Other;
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Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
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Qy 1 GluGinglylleValLeuProCysArgProGluGlylleProProAlaGluValGlu 20
Db 573 GAGCAGGCGCATCGTGTGCTGCCCTGCCCTCCACCGAGGGGCATCCCTCCACGCGGAGTGAG 632
Qy 21 TrpLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIleThrArg 40
Db 633 TGGCTCCGGACAGAGACCTGGTGGACCCGTCCTGGACCCCAATGTATCATCATCCGCGG 692
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 693 GAGCACAGCCTGGTGGTGGCGACAGCCCGCTTGTGTACACAGGCGCACTACACCTGGGTG 752
Qy 61 Ala 61
Db 753 GCC 755
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GenCore version 5.1.6
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Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

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17	94	28.8	3991	3	US-08-506-296B-3	Sequence 3, Appli
18	92.5	28.4	4548	4	US-08-571-479C-5	Sequence 5, Appli
19	88.5	27.1	5506	4	US-09-976-594-530	Sequence 530, App
20	87	26.7	5905	4	US-09-949-016-5625	Sequence 5625, Ap
21	87	26.7	6218	4	US-09-949-016-706	Sequence 706, App
22	87	26.7	6384	4	US-09-976-594-724	Sequence 724, App
23	87	26.7	6384	4	US-09-919-039-279	Sequence 279, App
24	85	26.1	6599	4	US-09-799-451-350	Sequence 350, App
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26	82	25.2	601	4	US-09-949-016-31728	Sequence 31728, A
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ALIGNMENTS

RESULT 1

US-08-808-982-1
; Sequence 1, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-808-982-1
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Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
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; Sequence 1, Application US/09306902A
; Patent No. 6272585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-306-902A-1
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Pred. No.: 6.23e-38 Length: 3014
Score: 326.00 Matches: 61
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Db 487 GAGCAGGCATTGTACTACCTTGTGCGCCCCCAGAGGAATCCCCCAGCTGAGGTGGAG 546
Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 547 TGGCTTCGAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATCACGCGG 606
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; Sequence 4794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; SOFTWARE: FastSeq for Windows Version 4.0
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; ORGANISM: Human
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Query Match: 74.23% Indels: 0
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; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
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; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-7

Alignment Scores:
Pred. No.:          9,06e-20      Length:      1659
Score:              201.00      Matches:      34
Percent Similarity: 79.31%      Conservative: 12
Best Local Similarity: 58.62%    Mismatches:  12
Query Match:        61.66%      Indels:       0
DB:                  4          Gaps:          0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-7 (1-1659)
Qy      4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db      526 ATTGTACTGCACTGCGCCACCAGAGGGAGTCCCTGTCGCGAGGTGGAATGCTGAAA 585
Qy      24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43
Db      586 AATGAAGAGCCCATTCGACTCTGAACAAGACGAGAACATTGACACCCAGGGCTGACCATTAAC 645
Qy      44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db      646 CTGATCATCAGGAGGACGGCTCTCGGACTCAGGAATAATACACCTGCATGGCA 699

RESULT 7
US-09-969-532-5
; Sequence 5, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1692
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-5

Alignment Scores:
Pred. No.:          9,3e-20      Length:      1692
Score:              201.00      Matches:      34
Percent Similarity: 79.31%      Conservative: 12
Best Local Similarity: 58.62%    Mismatches:  12
Query Match:        61.66%      Indels:       0
DB:                  4          Gaps:          0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-5 (1-1692)
Qy      4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db      526 ATTGTACTGCACTGCGCCACCAGAGGGAGTCCCTGTCGCGAGGTGGAATGCTGAAA 585
Qy      24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43
Db      586 AATGAAGAGCCCATTCGACTCTGAACAAGACGAGAACATTGACACCCAGGGCTGACCATTAAC 645
Qy      44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db      646 CTGATCATCAGGAGGACGGCTCTCGGACTCAGGAATAATACACCTGCATGGCA 699

RESULT 7
US-09-969-532-5
; Sequence 5, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1692
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-5

Alignment Scores:
Pred. No.:          9,3e-20      Length:      1692
Score:              201.00      Matches:      34
Percent Similarity: 79.31%      Conservative: 12
Best Local Similarity: 58.62%    Mismatches:  12
Query Match:        61.66%      Indels:       0
DB:                  4          Gaps:          0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-5 (1-1692)
Qy      4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db      526 ATTGTACTGCACTGCGCCACCAGAGGGAGTCCCTGTCGCGAGGTGGAATGCTGAAA 585
Qy      24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43
Db      586 AATGAAGAGCCCATTCGACTCTGAACAAGACGAGAACATTGACACCCAGGGCTGACCATTAAC 645
Qy      44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db      646 CTGATCATCAGGAGGACGGCTCTCGGACTCAGGAATAATACACCTGCATGGCA 699

RESULT 7
US-09-969-532-5
; Sequence 5, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1692
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-5

Alignment Scores:
Pred. No.:          9,37e-20     Length:      1701
Score:              201.00      Matches:      34
Percent Similarity: 79.31%      Conservative: 12
Best Local Similarity: 58.62%    Mismatches:  12
Query Match:        61.66%      Indels:       0
DB:                  4          Gaps:          0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-3 (1-1701)
Qy      4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db      526 ATTGTACTGCACTGCGCCACCAGAGGGAGTCCCTGTCGCGAGGTGGAATGCTGAAA 585
Qy      24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43
Db      586 AATGAAGAGCCCATTCGACTCTGAACAAGACGAGAACATTGACACCCAGGGCTGACCATTAAC 645
Qy      44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db      646 CTGATCATCAGGAGGACGGCTCTCGGACTCAGGAATAATACACCTGCATGGCA 699

RESULT 9
US-09-969-532-1
; Sequence 1, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1734
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-1
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```
Alignment Scores:
Pred. No.: 9.62e-20 Length: 1734
Score: 201.00 Matches: 34
Percent Similarity: 79.31% Conservatives: 12
Best Local Similarity: 58.62% Mismatches: 12
Query Match: 61.66% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-1 (1-1734)

Qy 4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db 526 ATTGTACTGCACCTGCCGCCACACAGAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAA 585

Qy 24 AsnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArgGluHisSer 43
Db 586 AATGAAGAGCCCATGTGACTCTGAACAAGACAGAGAACATTGACACAGGGCTGACCAATAAC 645

Qy 44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db 646 CTGATCATCAGCAGGACGGCTCTCGGACTCAGGAAATTACCTGCATGGCA 699

RESULT 10
US-09-969-532-15
; Sequence 15, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232e1 Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-969-532-15

Alignment Scores:
Pred. No.: 1.73e-19 Length: 2661
Score: 201.00 Matches: 34
Percent Similarity: 79.31% Conservatives: 12
Best Local Similarity: 58.62% Mismatches: 12
Query Match: 61.66% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-15 (1-2661)

Qy 4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db 526 ATTGTACTGCACCTGCCGCCACACAGAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAA 585

Qy 24 AsnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArgGluHisSer 43
Db 586 AATGAAGAGCCCATGTGACTCTGAACAAGACAGAGAACATTGACACAGGGCTGACCAATAAC 645

Qy 44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db 646 CTGATCATCAGCAGGACGGCTCTCGGACTCAGGAAATTACCTGCATGGCA 699

RESULT 11
US-09-969-532-13
; Sequence 13, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
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; TITLE OF INVENTION: No. 6777232e1 Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-969-532-13

Alignment Scores:
Pred. No.: 1.76e-19 Length: 2694
Score: 201.00 Matches: 34
Percent Similarity: 79.31% Conservatives: 12
Best Local Similarity: 58.62% Mismatches: 12
Query Match: 61.66% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-13 (1-2694)

Qy 4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db 526 ATTGTACTGCACCTGCCGCCACACAGAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAA 585

Qy 24 AsnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArgGluHisSer 43
Db 586 AATGAAGAGCCCATGTGACTCTGAACAAGACAGAGAACATTGACACAGGGCTGACCAATAAC 645

Qy 44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db 646 CTGATCATCAGCAGGACGGCTCTCGGACTCAGGAAATTACCTGCATGGCA 699

RESULT 12
US-09-969-532-11
; Sequence 11, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232e1 Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-969-532-11

Alignment Scores:
Pred. No.: 1.77e-19 Length: 2703
Score: 201.00 Matches: 34
Percent Similarity: 79.31% Conservatives: 12
Best Local Similarity: 58.62% Mismatches: 12
Query Match: 61.66% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-11 (1-2703)

Qy 4 IleValLeuProCysArgProProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db 526 ATTGTACTGCACCTGCCGCCACACAGAGGAGTCCCTGCTGCCGAGGTGGAATGGCTGAAA 585

Qy 24 AsnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArgGluHisSer 43
Db 586 AATGAAGAGCCCATGTGACTCTGAACAAGACAGAGAACATTGACACAGGGCTGACCAATAAC 645
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Db 586 AATGAAGAGCCATTGACTCTGAAACAGACAGAAACATTGACACCGGCTGACCATAC 645

Qy 44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61

Db 646 CTGATCATCAGCGAGGACCGCTCTCGGACTCAGGAAATACACCTGCATGGCA 699

RESULT 13

US-09-969-532-9

; Sequence 9, Application US/09969532

; Patent No. 6777232

; GENERAL INFORMATION:

; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin

; FILE REFERENCE: LEX-0244-USA

; CURRENT APPLICATION NUMBER: US/09/969,532

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 60/237,280

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 2736

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-969-532-9

Alignment Scores:

Pred. No.: 1.8e-19 Length: 2736

Score: 201.00 Matches: 34

Percent Similarity: 79.31% Conservative: 12

Best Local Similarity: 58.62% Mismatches: 12

Query Match: 61.66% Indels: 0

DB: 4 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-9 (1-2736)

Qy 4 IleValLeuProCysArgProGluGlyLeProGluValGluValGluTrpLeuArg 23

Db 526 ATTGTACTGACTGCCGCCACCCAGAGGAGTCCCTGCTGCCGAGGTGGATGCTGAAA 585

Qy 24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43

Db 586 AATGAAGAGCCATTGACTCTGAAACAGACAGAAACATTGACACCGGCTGACCATAC 645

Qy 44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61

Db 646 CTGATCATCAGCGAGGACCGCTCTCGGACTCAGGAAATACACCTGCATGGCA 699

RESULT 14

US-09-969-532-33

; Sequence 33, Application US/09969532

; Patent No. 6777232

; GENERAL INFORMATION:

; APPLICANT: Scoville, John

; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin

; FILE REFERENCE: LEX-0244-USA

; CURRENT APPLICATION NUMBER: US/09/969,532

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 60/237,280

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 33

; LENGTH: 3411

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-969-532-33

Alignment Scores:

Pred. No.: 2.44e-19 Length: 3411

Score: 201.00 Matches: 34

Percent Similarity: 79.31% Conservative: 12

Best Local Similarity: 58.62% Mismatches: 12

Query Match: 61.66% Indels: 0

DB: 4 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-969-532-33 (1-3411)

Qy 4 IleValLeuProCysArgProGluGlyLeProGluValGluValGluTrpLeuArg 23

Db 640 ATTGTACTGACTGCCGCCACCCAGAGGAGTCCCTGCTGCCGAGGTGGATGCTGAAA 699

Qy 24 AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43

Db 700 AATGAAGAGCCATTGACTCTGAAACAGACAGAAACATTGACACCGGCTGACCATAC 759

Qy 44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61

Db 760 CTGATCATCAGCGAGGACCGCTCTCGGACTCAGGAAATACACCTGCATGGCA 813

RESULT 15

US-09-949-016-16536

; Sequence 16536, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16536

; LENGTH: 114139

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)-(114139)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-16536

Alignment Scores:

Pred. No.: 1.19e-12 Length: 114139

Score: 170.00 Matches: 29

Percent Similarity: 88.37% Conservative: 9

Best Local Similarity: 67.44% Mismatches: 5

Query Match: 52.15% Indels: 0

DB: 4 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-949-016-16536 (1-114139)

Qy 19 ValGluTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIle 38

Db 29702 GTGGATGTTGAAAAATGAAGACATAAATGATCCCGTTGAAGATCGGAATTTTATATT 29761

Qy 39 ThrArgGluHisSerLeuValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThr 58

Db 29762 ACTATTGATCACAACCTCATCATATAAGCAGCCGCGACTCTCTGTACTGCNAATTACACC 29821

Qy 59 CysValAla 61

Db 29822 TGTGTTGCC 29830

Search completed: September 9, 2005, 09:50:52

Job time : 112.232 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 9, 2005, 04:41:16 ; Search time 608.726 Seconds
(without alignments)
658.098 Million cell updates/sec

Title: US-10-624-932c-2_COPY_163_223

Perfect score: 326

Sequence: 1 EQGIVLPCRPPEGIPPAEVE.....HSLVVRQARLADTANYTCVA 61

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10624932 @cgn 1.1 989 @runat_08092005_161709_15882
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	326	100.0	2752	10	US-09-918-779-1
3	326	100.0	2752	18	US-10-624-932-1
4	326	100.0	2881	10	US-09-970-944-1
5	326	100.0	3014	10	US-09-933-261-1
6	326	100.0	3014	14	US-10-256-702-1
7	326	100.0	3561	20	US-10-643-795A-77
8	326	100.0	3561	21	US-10-948-518-77
9	326	100.0	3580	17	US-10-311-623-13
10	230	70.6	2831	10	US-09-333-261-3
11	230	70.6	2831	14	US-10-256-702-3
12	230	70.6	2860	17	US-10-087-684-1
13	230	70.6	2860	17	US-10-087-684-3
14	230	70.6	2860	17	US-10-218-779-1
15	230	70.6	2860	17	US-10-218-779-3
16	230	70.6	2895	18	US-10-037-417-37
17	230	70.6	2995	11	US-09-972-211-55
18	230	70.6	2995	18	US-10-096-625-55
19	230	70.6	3485	9	US-09-816-828-18
20	230	70.6	3501	17	US-10-295-027-1123
21	230	70.6	3865	21	US-10-764-420-2213
22	230	70.6	3884	14	US-10-028-072-145
23	230	70.6	3884	14	US-10-140-808-145
24	230	70.6	3884	14	US-10-121-049-145
25	230	70.6	3884	14	US-10-123-904-145
26	230	70.6	3884	14	US-10-140-470-145
27	230	70.6	3884	14	US-10-175-746-145
28	230	70.6	3884	14	US-10-176-918-145
29	230	70.6	3884	14	US-10-176-921-145
30	230	70.6	3884	14	US-10-137-865-145
31	230	70.6	3884	14	US-10-140-474-145
32	230	70.6	3884	14	US-10-142-431-145
33	230	70.6	3884	14	US-10-143-114-145
34	230	70.6	3884	14	US-10-142-419-145
35	230	70.6	3884	14	US-10-123-262-145
36	230	70.6	3884	14	US-10-142-423-145
37	230	70.6	3884	14	US-10-121-050-145
38	230	70.6	3884	14	US-10-141-755-145
39	230	70.6	3884	14	US-10-143-032-145
40	230	70.6	3884	14	US-10-123-108-145
41	230	70.6	3884	14	US-10-123-236-145
42	230	70.6	3884	14	US-10-140-921-145
43	230	70.6	3884	14	US-10-140-928-145
44	230	70.6	3884	14	US-10-140-928-145
45	230	70.6	3884	14	US-10-121-045-145

ALIGNMENTS

RESULT 1
US-10-240-154-15
; Sequence 15, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKEW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240,154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 2697

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; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15

Alignment Scores:
Pred. No.: 7,94e-37 Length: 2697
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-624-932c-2_COPY_163_223 (1-61) x US-10-240-154-15 (1-2697)

QY 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
DB 487 GAGCAGGCGCATGTGACTTGTGCGCCCCCAGAGAGATCCCCCAGCTGAGGTGGAG 546

QY 21 TrpLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIleThrArg 40
DB 547 TGGCTTCGAAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGCTATCATCACGCGG 606

QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAenTyrThrCysVal 60
DB 607 GAGCACAGCCTAGTCGTGCGTCAGGCGCGCTGCGCCGACACACGCGCAACTACACCTGTGTG 666

QY 61 Ala 61
DB 667 GCC 669

RESULT 2
US-09-918-779-1
; Sequence 1, Application US/09918779
; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 2001-07-28
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08

; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-779-1

Alignment Scores:
Pred. No.: 8,13e-37 Length: 2752
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-624-932c-2_COPY_163_223 (1-61) x US-09-918-779-1 (1-2752)

QY 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
DB 532 GAGCAGGCGCATGTGCTGCTGCCCTCCACCCGAGGCGCATCCCTCCAGCGAGGTGGAG 591

QY 21 TrpLeuArgAenGluAspLeuValAspProSerLeuAspProAenValTyrIleThrArg 40
DB 592 TGGCTCCGGAACGAGGACCTGCTGGACCCGCTGCGCCCAATGTATACATCACGCGG 651

QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAenTyrThrCysVal 60
DB 652 GAGCACAGCCTGCTGGTGGTGACAGGCGCCCTTGTCTGACACGCGCAACTACCTGCTGTG 711

QY 61 Ala 61
DB 712 GCC 714

RESULT 3
US-10-624-932-1
; Sequence 1, Application US/10624932
; Publication No. US20040096877A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/10/624,932
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; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918,779
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-624-932-1

Alignment Scores:
Pred. No.: 8.13e-37 Length: 2752
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-10-624-932-1 (1-2752)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Db 532 GAGCAGGGGATCGTGGCTGCCCTCCCGGAGGCGCATCCCTCCAGCCGAGGTGGAG 591

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 592 TGGCTCCGGACGAGGACCTGGTGACCCGTCCTGGACCCCAATGTATACATCAGCGG 651

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 652 GAGCACAGCCTGGTGGTGGACAGCGCCGCTTGTGTGACAGCGGCAACTACACCTGCGTG 711

Qy 61 Ala 61
Db 712 GCC 714

RESULT 4
US-09-970-944-1
; Sequence 1, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same an
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 1
; LENGTH: 2881
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-944-1

Alignment Scores:
Pred. No.: 8.58e-37 Length: 2881
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-09-970-944-1 (1-2881)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Db 573 GAGCAGGGGATCGTGGCTGCCCTCCCGGAGGCGCATCCCTCCAGCCGAGGTGGAG 632

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 633 TGGCTCCGGACGAGGACCTGGTGACCCGTCCTGGACCCCAATGTATACATCAGCGG 692

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 693 GAGCACAGCCTGGTGGTGGACAGCGCCGCTTGTGTGACAGCGGCAACTACACCTGCGTG 752

Qy 61 Ala 61
Db 753 GCC 755

RESULT 5
US-09-933-261-1
; Sequence 1, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
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;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-933-261-1
Alignment Scores:
Pred. No.: 9.05e-37 Length: 3014
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_163_223 (1-61) x US-09-933-261-1 (1-3014)
QY 1 GluGlnGlyLeuValLeuProCysArgProGluGlyLeuProAlaGluValGlu 20
Db 487 GAGCAGGCAATTGTACTTGTGCGCCCCCAGAGGAGTCCCCCAGCTGAGGTGAG 546
QY 21 TrpLeuArgGlnAspLeuValAspProSerLeuAspProAenValTyrIleThrArg 40
Db 547 TGGCTTCGAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATCACGCGG 606
QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAenTyrThrCysVal 60
Db 607 GAGCACAGCCTAGTGTGCGGTGAGCGCCGCTGCGCCGACACGCGCAACTACACTGTGTG 666
QY 61 Ala 61
Db 667 GCC 669
RESULT 6
US-10-256-702-1
; Sequence 1, Application US/10256702
; Publication No. US20030059859A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/256,702
; FILING DATE: 27-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-256-702-1
Alignment Scores:
Pred. No.: 9.05e-37 Length: 3014
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-624-932C-2_COPY_163_223 (1-61) x US-10-256-702-1 (1-3014)
QY 1 GluGlnGlyLeuValLeuProCysArgProGluGlyLeuProAlaGluValGlu 20
Db 487 GAGCAGGCAATTGTACTTGTGCGCCCCCAGAGGAGTCCCCCAGCTGAGGTGAG 546
QY 21 TrpLeuArgGlnAspLeuValAspProSerLeuAspProAenValTyrIleThrArg 40
Db 547 TGGCTTCGAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATCACGCGG 606
QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAenTyrThrCysVal 60
Db 607 GAGCACAGCCTAGTGTGCGGTGAGCGCCGCTGCGCCGACACGCGCAACTACACTGTGTG 666
QY 61 Ala 61
Db 667 GCC 669
RESULT 7
US-10-643-795A-77
; Sequence 77, Application US/10643795A
; Publication No. US20040241703A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/643,795A
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-643-795A-77
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Alignment Scores:
Pred. No.: 1,1e-36 Length: 3561
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps:

US-10-624-932C-2_COPY_163_223 (1-61) x US-10-643-795A-77 (1-3561)

Qy 1 GluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGlu 20
Db 490 GAGCAGGGCATCGTGTGCCCTCCACCGAGGGATCCCTCCAGCGAGTGAG 549

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTrpThrArg 40
Db 550 TGGCTCCGGAAACGAGGACCTGGTGGACCGCTCCCTGGACCCCAATTGATACATCACGCGG 609

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrrThrCysVal 60
Db 610 GAGCAGACCTGGTGGTGGACAGCGCCGCTTCCTGGACCCCAATTGATACATCACGCGG 669

Qy 61 Ala 61
Db 670 GCC 672

RESULT 8
US-10-948-518-77
; Sequence 77, Application US/10948518
; Publication No. US20050064492A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/948,518
; PRIOR FILING DATE: 2004-09-22 60/413,192
; PRIOR APPLICATION NUMBER: US/10/643,795
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-948-518-77

Alignment Scores:
Pred. No.: 1,1e-36 Length: 3561
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-10-948-518-77 (1-3561)

Qy 1 GluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGlu 20
Db 490 GAGCAGGGCATCGTGTGCCCTCCACCGAGGGATCCCTCCAGCGAGTGAG 549

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTrpThrArg 40
Db 550 TGGCTCCGGAAACGAGGACCTGGTGGACCGCTCCCTGGACCCCAATTGATACATCACGCGG 609

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrrThrCysVal 60
Db 610 GAGCAGACCTGGTGGTGGACAGCGCCGCTTCCTGGACCCCAATTGATACATCACGCGG 669

Qy 61 Ala 61
Db 670 GCC 672

RESULT 9
US-10-311-623-13
; Sequence 13, Application US/10311623
; Publication No. US20040023244A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Dannie B.
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.
; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
; APPLICANT: LU, Duong Aina M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.
; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: EP-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 3580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/key: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CBI
US-10-311-623-13

Alignment Scores:
Pred. No.: 1,11e-36 Length: 3580
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps:

US-10-624-932C-2_COPY_163_223 (1-61) x US-10-311-623-13 (1-3580)

Qy 1 GluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGlu 20


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Score: 230.00 Matches: 38
Percent Similarity: 87.93% Conservative: 13
Best Local Similarity: 65.52% Mismatches: 7
Query Match: 70.55% Indels: 0
DB: 17 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-10-087-684-3 (1-2860)

Qy 4 IleValLeuProCysArgProGluGlyLeProAlaGluValGluTrpLeuArg 23
Db 566 GTTCTCTGAGTGCCTGCGGAGGGGTGCTGTGCGGAGGTGAATGCTCAAG 625

Qy 24 AsnGluAspLeuValAspProSerLeuAspProHsnValTrpLeuArgGluHisSer 43
Db 626 AATGAGGATGTCATCGACCCGCCAGGACACCAACTTCCTGCTCACCATCGACCAAC 685

Qy 44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTrpThrCysValAla 61
Db 686 CTCATCATCGCCAGGCGCGCTGTGCGACACTGCCAACTATACCTCGTGGCC 739

RESULT 14
US-10-218-779-1
; Sequence 1, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zerkhusen, Bryan
; APPLICANT: Malvankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; CURRENT APPLICATION NUMBER: US/10/218,779
; PRIOR FILING DATE: 2002-08-14
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-218-779-1

Score: 230.00 Matches: 38
Percent Similarity: 87.93% Conservative: 13
Best Local Similarity: 65.52% Mismatches: 7
Query Match: 70.55% Indels: 0
DB: 17 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x US-10-087-684-3 (1-2860)

Qy 4 IleValLeuProCysArgProGluGlyLeProAlaGluValGluTrpLeuArg 23
Db 566 GTTCTCTGAGTGCCTGCGGAGGGGTGCTGTGCGGAGGTGAATGCTCAAG 625

Qy 24 AsnGluAspLeuValAspProSerLeuAspProHsnValTrpLeuArgGluHisSer 43
Db 626 AATGAGGATGTCATCGACCCGCCAGGACACCAACTTCCTGCTCACCATCGACCAAC 685

Qy 44 LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTrpThrCysValAla 61
Db 686 CTCATCATCGCCAGGCGCGCTGTGCGACACTGCCAACTATACCTCGTGGCC 739

RESULT 15
US-10-218-779-3
; Sequence 3, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zerkhusen, Bryan
; APPLICANT: Malvankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; CURRENT APPLICATION NUMBER: US/10/218,779
; PRIOR FILING DATE: 2002-08-14
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2000-11-29
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 2001-08-20
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-218-779-3
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-218-779-3

Alignment Scores:
Pred. No.:      8,43e-23      Length:      2860
Score:          230.00      Matches:      38
Percent Similarity: 87.93%      Conservative: 13
Best Local Similarity: 65.52%      Mismatches:  7
Query Match:     70.55%      Indels:      0
DB:              17          Gaps:      0

US-10-624-932C-2_COPY_163_223 (1-61) x US-10-218-779-3 (1-2860)

Qy  4  IleValLeuProCysArgProGluGlyIleProProAlaGluValGluTrpLeuArg 23
Db  566 GTTCTCTGTCAGTGCCTGCGCGGAGGGGTGCTGTGGCCGAGGTGGAATGGCTCAAG 625

Qy  24  AsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArgGluHisSer 43
Db  626 AATGAGGATGTCATCGACCCGCCAGGACACCAACTTCTCTGCTCACCATCGACCAAC 685

Qy  44  LeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysValAla 61
Db  686 CTCATCATCCGCCAGGCCCGCTGTCGACACTGCCCAACTATACCTGGTGCC 739
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Search completed: September 9, 2005, 18:52:05
Job time : 616.726 secs

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GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 22:38:37; Search time 2007.62 Seconds
(without alignments)
1156.553 Million cell updates/sec

Title: US-10-624-932C-2_COPY_163_223

Perfect score: 326

Sequence: 1 EQGIVLPCRPPEGIPPAEVE.....HSLVVRQARLADTANYTCVA 61

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/cgn2_1/USFTO_spool_h/US10624932/runat_08092005_161706_15792/app_query.fasta_1.1386
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-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CGN 1.1.8180 @runat_08092005_161706_15792 -NCPUS=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -TRANS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gssi:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	326	100.0	421	6	CB764405 AMGNNUC:N
2	326	100.0	445	6	CB744716 AMGNNUC:N
3	326	100.0	471	5	BX282095 BX282095
4	326	100.0	514	5	BX522364 BX522364
5	326	100.0	749	7	CF735417 UI-M-HBO-
6	326	100.0	751	7	CF735550 UI-M-HBO-
7	326	100.0	818	4	B1818609 60303362
8	326	100.0	1175	2	BFS30640 602071931
9	326	100.0	1532	3	BC033727 Homo sapi

10	322	98.8	485	6	CB727042
11	320	98.2	1034	4	B1758231
12	318	97.5	853	5	BX364574
13	313	96.0	276	1	AA288582
14	313	96.0	723	5	BU613458
15	299	91.7	843	4	BG913440
16	283	86.8	900	5	BX345406
17	270	82.8	548	5	BX452510
18	245	75.2	3790	3	AK031655
19	242	74.2	459	2	BE700724
20	242	74.2	841	5	BP435136
21	242	74.2	856	7	CN164143
22	242	74.2	1843	3	BC034747
23	242	74.2	2802	9	AY406491
24	241	73.9	720	1	AI959236
25	236	72.4	351	1	AJ729962
26	230	70.6	403	2	AW357482
27	230	70.6	517	1	AI508226
28	230	70.6	523	5	BX526679
29	230	70.6	679	7	CO045001
30	230	70.6	2532	9	AY411747
31	230	70.6	2532	9	AY411749
32	230	70.6	3866	3	AK018177
33	223	68.4	594	6	CA771550
34	221	67.8	977	5	BX345407
35	215	66.0	373	1	AA020206
36	215	66.0	1072	5	BX422753
37	213	65.3	2802	9	AY406492
38	208	63.8	774	5	BU365958
39	202	62.0	2791	9	AY406493
40	201	61.7	733	5	BX920046
41	201	61.7	2775	9	AY401469
42	201	61.7	2775	9	AY401471
43	195	59.8	2507	9	AY401470
44	192	58.9	445	5	BX291669
45	190	58.3	693	6	CB246544

ALIGNMENTS

RESULT 1

CB764405

LOCUS

DEFINITION

nrhy7-00021-f2 5', mRNA sequence.

ACCESSION

CB764405

VERSION

CB764405.1

KEYWORDS

EST.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

REFERENCE

1 (bases 1 to 421)

AUTHORS

Amgen EST Program

TITLE

Amgen Rat EST Program

JOURNAL

Unpublished (2003)

COMMENT

Contact: Dan Fitzpatrick

FEATURES

Location/Qualifiers

1. 421

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="nrhy7-00021-f2"

/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat

hypothesis adult female Wistar rat avg. Insert size 2.3

kb fraction 6 and 7"

ORIGIN

CB764405 421 bp mRNA linear EST 16-MAY-2003
AMGNNUC:NRHY7-00021-F2-A nrhy7 (10850) Rattus norvegicus cDNA clone
nrhy7-00021-f2 5', mRNA sequence.

CB764405

CB764405.1

EST.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 421)

Amgen EST Program

Amgen Rat EST Program

Unpublished (2003)

Contact: Dan Fitzpatrick

Amgen, Inc.

One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881

Plate: 00021 row: f column: 2.

Location/Qualifiers

1. 421

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="nrhy7-00021-f2"

/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat

hypothesis adult female Wistar rat avg. Insert size 2.3

kb fraction 6 and 7"

ORIGIN

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Alignment Scores:
Pred. No.: 7,85e-31 Length: 421
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x CB764405 (1-421)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db 191 GAGCAAGGCATTGTACTACCTTGTGCGCCCGCCAGAGGAATCCCCCAGCTGAGGTGGAG 240

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 241 TGGCTTCCGAATGAGGACCTCGTGACCCCTCCCTCGATCCCAATGTGTACATCACGCGG 300

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 301 GAGCACAGCCTAGTGTGCGTCAGCGCCGCTGGCCGACACGGCCAACTACACCTGTGTG 360

Qy 61 Ala 61
Db 361 GCC 363

RESULT 2
CB744716
LOCUS CB744716 445 bp mRNA linear EST 11-APR-2003
DEFINITION AMGNNUC:NRHZ1-00003-e12-A nrhz1 (10741) Rattus norvegicus CDNA
ACCESSION CB744716
VERSION CB744716.1 GI:29812016
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 445)
AUTHORS Angen EST Program.
TITLE Angen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00003 row: e column: 12.
FEATURES
Location/Qualifiers
source 1..445
/organism="Rattus norvegicus"
/mol_type="mRNA"
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/clone="nrhz1-00003-e12"
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/clone_lib="nrhz1 (10741)"
/notes="Vector: pSPORT1; Site_1: SalI; Site_2: NotI;
hypothalamus"
ORIGIN
Alignment Scores:
Pred. No.: 8,36e-31 Length: 445
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x CB744716 (1-445)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProProAlaGluValGlu 20
Db 191 GAGCAAGGCATTGTACTACCTTGTGCGCCCGCCAGAGGAATCCCCCAGCTGAGGTGGAG 240

Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
Db 241 TGGCTTCCGAATGAGGACCTCGTGACCCCTCCCTCGATCCCAATGTGTACATCACGCGG 300

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
Db 301 GAGCACAGCCTAGTGTGCGTCAGCGCCGCTGGCCGACACGGCCAACTACACCTGTGTG 360

Qy 61 Ala 61
Db 361 GCC 363

RESULT 2
CB744716
LOCUS CB744716 471 bp mRNA linear EST 04-MAR-2003
DEFINITION BX282095 NCI CGAP Brn67 Homo sapiens cDNA clone IMAGE998J0610886 ;
IMAGE:4943333, mRNA sequence.
ACCESSION BX282095
VERSION BX282095.1 GI:28612897
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 471)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
HUMAN UNIGENESET - RZPD3
Unpublished (2003)
CONTACT: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE998J0610886.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl/cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13u, Primer sequence: CGTTGTAACGACGCGCCAGT.
FEATURES
Location/Qualifiers
source 1..471
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE998J0610886 ; IMAGE:4943333"
/tissue_type="anaplastic oligodendroglioma with lp/19q
loss"
/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Brn67"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."
ORIGIN
Alignment Scores:
Pred. No.: 8,93e-31 Length: 471
Score: 326.00 Matches: 61
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x BX282095 (1-471)
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US-10-624-932C-2_COPY_163_223 (1-61) x BX522364 (1-514)

QY	1	GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu	20
DB	5	GAGCAAGCATTTGTCTACCTTGTGCGCCCCGGAAGGAATCCCCCAGCTGAGGTGGAG	64
QY	21	TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg	40
DB	65	TGGCTCCGAAATAGGAGACCTCGTGGACCCCTCCCTCGACCCCAATGTGTACATCACACGG	124
QY	41	GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal	60
DB	125	GAGCACACCTTAGTCTGTGGCGAGCCCGCGCTGGCGACACTGCCAACTACACCTCGCGTG	184
QY	61	Ala 61	
DB	185	GCC 187	

RESULT 5	CF735417	749 bp	linear	EST 10-OCT-2003
LOCUS	UI-M-HBO-cke-a-07-0-UT.r1 NTH_EMAP_HBO		Mus musculus	CDNA clone
DEFINITION	IMAGE:30549030 5', mRNA sequence.			
ACCESSION	CF735417			
VERSION	CF735417.1			
KEYWORDS	GI:37631753			
SOURCE	EST.			
ORGANISM	Mus musculus (house mouse)			
	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 749)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: ccabbs-r@mail.nih.gov			

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FEATURES
source
seq primer
Location/Qualifiers
1..749
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30549030"
/tissue_type="whole eye"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP HB0"

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ORIGIN	Alignment Scores:	Length:
Origo di. 8.30ptc embryo.5. pcwv-5f0k12 vector.	Pred. No.: 9.88e-31	514
	Score: 326.00	Matches: 61
	Percent Similarity: 100.00%	Conservative: 0
	Best Local Similarity: 100.00%	Mismatches: 0

DB:	2	0
caps:	2	0
Alignment Scores:		

Pred. No.: 1.53e-30 Length: 749
 Score: 326.00 Matches: 61
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-624-932c-2_COPY_163_223 (1-61) x CF735417 (1-749)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProGluGlyIleProAlaGluValGlu 20
 |||||
 Db 258 GAGCAAGGCAATGTGTACCTGTGCGCCCGGGAAGGAATCCCCAGCTGAGGTGGAG 317
 |||||

Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArg 40
 |||||

Db 318 TGGCTCCGAAATGAGGACCTGTCGACCCCTCCCTCGACCCCAATGTGTACATCACACGG 377
 |||||

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
 |||||

Db 378 GAGCACACCTAGTCGTGCGGAGGCCCGCTGCGGACACTGCCAACTACACTGCTGGTG 437
 |||||

Qy 61 Ala 61
 |||||

Db 438 GCC 440

RESULT 6
 CF735550
 LOCUS
 DEFINITION UI-M-HB0-cke-i-06-0-UI.r1 NIH_BMAP_HB0 Mus musculus cDNA clone
 IMAGE:30549221 5', mRNA sequence.

ACCESSION CF735550
 VERSION CF735550.1 GI:37631886
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 751)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. James Lin University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousef1.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pYX-5.
 Location/Qualifiers
 1..751
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30549221"
 /tissue_type="whole eye"
 /dev_stages="embryo 12.5,13.5,14.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_HB0"
 /note="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail

is TTATTGAAGT. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH).

ORIGIN

Alignment Scores:
 Pred. No.: 1.53e-30 Length: 751
 Score: 326.00 Matches: 61
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-624-932c-2_COPY_163_223 (1-61) x CF735550 (1-751)

Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProGluGlyIleProAlaGluValGlu 20
 |||||

Db 257 GAGCAAGGCAATGTGTACCTGTGCGCCCGGGAAGGAATCCCCAGCTGAGGTGGAG 316
 |||||

Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProAnValTyrIleThrArg 40
 |||||

Db 317 TGGCTCCGAAATGAGGACCTGTCGACCCCTCCCTCGACCCCAATGTGTACATCACACGG 376
 |||||

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
 |||||

Db 377 GAGCACACCTAGTCGTGCGGAGGCCCGCTGCGGACACTGCCAACTACACTGCTGGTG 436
 |||||

Qy 61 Ala 61
 |||||

Db 437 GCC 439

RESULT 7
 B1818609
 LOCUS
 DEFINITION 603033362F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174559 5',
 mRNA sequence.

ACCESSION B1818609
 VERSION B1818609.1 GI:15929902
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 818)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LUAM1434 row: 1 column: 16
 High quality sequence stop: 744.
 Location/Qualifiers
 1..818
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5174559"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_115"
 /note="Organ: pooled brain, lung, testis; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,

FEATURES
 source

insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 1.69e-30 Length: 818
 Score: 326.00 Matches: 61
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x B1818609 (1-818)

QY 1 GluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGlu 20
 Db 490 GAGCAGGCGATCGTCTGCCCTGCCGTCCACGGAGGCGATCCCTCCAGCCGAGGTGGAG 549

QY 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
 Db 550 TGGCTCCGGAACGAGGACCTGGTGGACCCGTCCTCGACCCCAATGTATACATCACCGG 609

QY 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
 Db 610 GAGCACAGCCTGGTGGTGGCAGACGGCCGCTTCTGCACACGGCCAACTACACCTGCGTG 669

QY 61 Ala 61
 Db 670 GCC 672

RESULT 8
 BF530640 1175 bp mRNA linear EST 11-DEC-2000
 LOCUS 602071931F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4214959
 DEFINITION 5', mRNA sequence.

ACCESSION BF530640
 VERSION BF530640.1 GI:11618003
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1175)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-rc@mail.nih.gov
 Tissue procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM9789 row: m column: 08
 High quality sequence stop: 665.
 Location/Qualifiers
 1..1175
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4214959"
 /tissue_type="anaplastic oligodendroglioma with 1p/19q
 loss"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI_CGAP_Brn67"
 /notes="Organ: Brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 2.3 kb. Constructed by Life
 Technologies. Note: this is a NCI CGAP Library."

FEATURES
 source

Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
 Maduro, O.L., Masiello, C., Maekeri, B., Mastrian, S.D., McGloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 68 Row: i Column: 2
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Genomescan gene prediction
 This clone has the following problem: frame shifted.

FEATURES

source
 1. 1532
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5166762"
 /tissue types="Brain, adult medulla"
 /clone_lib="NIH_MGC_119"
 /lab_host="DH10B"
 /note="vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:
 Pred. No.: 3,49e-30 Length: 1532
 Score: 326.00 Matches: 61
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x BC033727 (1-1532)

Qy 1 GluGlnGlyLeValLeuProCysArgProGluGlyLeProProAlaGluValGlu 20
 |||||
 Db 807 GAGCAGGCGCATCGTGTGCTGCGCTCCACCGGAGGCGCATCCCTCCAGCGCGAGGTGGAG 865

Qy 21 TrpLeuArgGlnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
 |||||
 Db 867 TGGCTCCGGACACGAGGACCTGGTGACCGGCTCCCTGGACCCCAATGATATACATCACCGGG 926

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
 |||||
 Db 927 GAGCACAGCTGTGTGGTGGCAGACGCGCGCTTCTGACACGGCCCAACTACACCTGGTG 985

Qy 61 Ala 61
 |||||
 Db 987 GCC 989

RESULT 10

LOCUS CB727042 485 bp mRNA linear EST 11-APR-2003
 DEFINITION AMGNNUC:NRHVS-00009-C10-A W Rat hypothalamus (10471) Rattus
 norvegicus cDNA clone nrhys-00009-c10 5', mRNA sequence.
 ACCESSION CB727042
 VERSION CB727042.1 GI:29794027
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE 1 (bases 1 to 485)
 AUTHORS Angen EST Program.
 TITLE Angen Rat EST Program
 JOURNAL Unpublished (2003)
 COMMENT Contact: Dan Fitzpatrick
 Angen, Inc
 One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00009 row: c column: 10.
 Location/Qualifiers

FEATURES

source
 1. 485
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="nrhys-00009-c10"
 /notes="Vector: pSPORT1, Site 1: SalI; Site 2: NotI; W Rat
 hypothalamus adult female WiStar rat avg. Insert size 2.3
 kb fraction 6 and 7"

ORIGIN

Alignment Scores:
 Pred. No.: 2,94e-30 Length: 485
 Score: 322.00 Matches: 60
 Percent Similarity: 98.36% Conservative: 0
 Best Local Similarity: 98.36% Mismatches: 1
 Query Match: 98.77% Indels: 0
 DB: 6 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x CB727042 (1-485)

Qy 1 GluGlnGlyLeValLeuProCysArgProGluGlyLeProProAlaGluValGlu 20
 |||||
 Db 236 GAGCAAGGCATTGTACTACCTTGTGCCCCCAAGAGAAATCCCCAGCTGAGGTGGAG 295

Qy 21 TrpLeuArgGlnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
 |||||
 Db 296 TGGCTTCGAATGAGGACCTCGTGGACCCCTCCCTCGATCCCAATGTGTACATCACCGGG 355

Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
 |||||
 Db 356 GAGCACAGCTGTGTGGTGGCAGCGCGCTTCTGACACGGCCCAACTACACCTGTGTG 415

Qy 61 Ala 61
 |||||
 Db 416 GCC 418

RESULT 11

LOCUS B1758231 1034 bp mRNA linear EST 25-SEP-2001
 DEFINITION 603029876F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5200171 5',
 mRNA sequence.
 ACCESSION B1758231
 VERSION B1758231.1 GI:15749809
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1034)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: sgabbs@email.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

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Plate: LAM11501 row: g column: 20
High quality sequence stop: 793.
FEATURES
  source
    1..1034
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:5200171"
      /lab_host="DH10B"
      /clone_lib="NIH_MGC_114"
      /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
  Alignment Scores:
    Pred. No.: 1..26e-29 Length: 1034
    Score: 320.00 Matches: 60
    Percent Similarity: 98.36% Conservative: 0
    Best Local Similarity: 98.36% Mismatches: 1
    Query Match: 98.16% Indels: 0
    DB: 4 Gaps: 0
  US-10-624-932C-2_COPY_163_223 (1-61) x B1758231 (1-1034)
  Qy 1 GluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGlu 20
  Db 383 GAGCAGGCGCATCGTCTGCTCCCTGCGTCCACCGGAGGCGCATCCCTCCAGCGAGGTGGAG 442
  Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
  Db 443 TGGCTCCGGAACGAGGACCTGGTGACCGCTCCCTGGACCCCAATGTATACATCACGCGG 502
  Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCysVal 60
  Db 503 GAGCACAGCCTGGTGGTGGCGAGCGCCGCTTGTGTGACGGCAACTACATCACCTCGGTG 562
  Qy 61 Ala 61
  Db 563 GCC 565
  RESULT 12
  LOCUS BX364574 853 bp mRNA linear EST 08-APR-2004
  DEFINITION BX364574 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DC023YB10 5-PRIME, mRNA sequence.
  ACCESSION BX364574
  VERSION BX364574.2 GI:46286957
  KEYWORDS EST.
  SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1. (bases 1 to 853)
  Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
  Full-length cDNA libraries and normalization
  Unpublished (2001)
  On May 5, 2003 this sequence version replaced gi:30368812.
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
  Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
```

```
3529.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS1AC006ZF06QPI&c=3529.f.
FEATURES
  source
    1..853
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="CS0DC023YB10"
      /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
      /clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
      /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
  ORIGIN
  Alignment Scores:
    Pred. No.: 1.79e-29 Length: 853
    Score: 318.00 Matches: 59
    Percent Similarity: 100.00% Conservative: 0
    Best Local Similarity: 100.00% Mismatches: 0
    Query Match: 97.55% Indels: 0
    DB: 5 Gaps: 0
  US-10-624-932C-2_COPY_163_223 (1-61) x BX364574 (1-853)
  Qy 1 GluGlnGlyIleValLeuProCysArgProProGluGlyIleProProAlaGluValGlu 20
  Db 675 GAGCAGGCGCATCGTCTGCTCCCTGCGTCCACCGGAGGCGCATCCCTCCAGCGAGGTGGAG 734
  Qy 21 TrpLeuArgAnGluAspLeuValAspProSerLeuAspProAsnValTyrIleThrArg 40
  Db 735 TGGCTCCGGAACGAGGACCTGGTGACCGCTCCCTGGACCCCAATGTATACATCACGCGG 794
  Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnTyrThrCys 59
  Db 795 GAGCACAGCCTGGTGGTGGCGACGCGCCCTTGTGTGACGCGCAACTACACCTGC 851
  RESULT 13
  LOCUS AA288582 276 bp mRNA linear EST 14-APR-1997
  DEFINITION mp15g05.r1 Life Tech mouse embryo 8 5dpc 10664019 Mus musculus CDNA clone IMAGE:569336 5', similar to TR:E67610 E67610 UNC-5', mRNA sequence.
  ACCESSION AA288582
  VERSION AA288582.1 GI:1937649
  KEYWORDS EST.
  SOURCE Mus musculus (house mouse)
  ORGANISM Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1. (bases 1 to 276)
  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
  The WashU-HMI Mouse EST Project
  Unpublished (1996)
  Contact: Marra M/Mouse EST Project
  WashU-HMI Mouse EST Project
  Washington University School of MedicineP
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: mouseest@watson.wustl.edu
  This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
  MGI:343984
  Seq primer: -28m13 rev1 ET from Amersham
  High quality sequence stop: 271.
  Location/Qualifiers
  FEATURES
```

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source
1. .276
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAG8:569336"
/tissue_type="embryo"
/dev_stage="8.5dpc embryos"
/lab_hosts="DHI08"
/notes="Organ: whole embryo; Vector: pCMV-SPORT2; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. -8.5dpc embryos. pCMV-SPORT2 vector."

ORIGIN
Alignment Scores:
Pred. No.: 2,07e-29 Length: 276
Score: 313.00 Matches: 61
Percent Similarity: 98.39% Conservative: 0
Best Local Similarity: 98.39% Mismatches: 0
Query Match: 96.01% Indels: 1
DB: 1 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x AA288582 (1-276)
Qy 1 GluGlnGlyIleValLeuProCysArgProGluGlyIleProAlaGluValGlu 20
Db 4 GAGCAGGCGATTTGCTACCTTGTGCGCCCGCGGAGGAATCCCCCGAGCTGAGGTGGAG 63
Qy 21 TrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValThrArg 40
Db 64 TGGCTCCGAATGAGGACCTGTGCGACCCCTCCCTCGACCCCATGTGTACATCACACGG 123
Qy 41 GluHisSerLeuValValArgGlnAlaArgLeuAlaAsp-ThrAlaAsnThrCysVa 60
Db 124 GAGCACAGCCTAGTGTGTCGCGCGAGCGCCGCTGCGCGACTACTGCCAACTACACCTCGT 183
Qy 60 lAla 61
Db 184 GGCC 187

RESULT 14
LOCUS BU613458 723 bp mRNA linear EST 20-FEB-2003
DEFINITION UI-M-EWO-caz-d-10-0-UI.r1 NIH_BMAP_EWO Mus musculus cDNA clone
ACCESSION BU613458
VERSION BU613458.1 GI:23279673
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 723)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1. .723
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"

FEATURES
source
/db_xref="taxon:10090"
/clone="UI-M-EWO-caz-d-10-0-UI"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_hosts="DHI08 (T1 phage resistant)"
/clone_lib="NIH_BMAP_EWO"
/notes="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
Alignment Scores:
Pred. No.: 6.29e-29 Length: 723
Score: 313.00 Matches: 61
Percent Similarity: 98.39% Conservative: 0
Best Local Similarity: 98.39% Mismatches: 0
Query Match: 96.01% Indels: 1
DB: 5 Gaps: 0

US-10-624-932C-2_COPY_163_223 (1-61) x BU613458 (1-723)
Qy 1 GluGlnGlyIleValLeuProCysArgProPro-GluGlyIleProAlaGluValGlu 20
Db 149 GAGCAGGCGATTTGCTACCTTGTGCGCCCGCGGAGGAATCCCCCGAGCTGAGGTGGGA 208
Qy 20 uTrpLeuArgAsnGluAspLeuValAspProSerLeuAspProAsnValThrArg 40
Db 209 GTGGCTCCGAATGAGGACCTGTGAGACCCCTCCCTCGACCCCATGTGTACATCACAG 268
Qy 40 gGluHisSerLeuValValArgGlnAlaArgLeuAlaAspThrAlaAsnThrCysVa 60
Db 269 GGAGCACAGCCTAGTGTGTCGCGCGAGCGCCGCTGCGCGACACTGCCAACTACACCTCGT 328
Qy 60 lAla 61
Db 329 GGCC 332

RESULT 15
LOCUS BG913440 843 bp mRNA linear EST 05-JUN-2001
DEFINITION 602811321F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4943333
ACCESSION BG913440
VERSION BG913440.1 GI:14293916
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 843)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

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ORIGIN

Search completed: September 9, 2005, 04:40:32
Job time : 2013.62 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:47:02 ; Search time 4861.88 Seconds
(without alignments)
1166.064 Million cell updates/sec

Title: US-10-624-932C-2_COPY_232_348

Perfect score: 682

Sequence: 1 SASAAVIVYVVGWSTWTEW.....NGBECQGTDLDRNCTSDL 117

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=biolum62 -TRANS=human40.cdi -LIST=45
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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	682	100.0	2697	6	AX451652 Sequence
2	682	100.0	2752	6	AX449572 Sequence
3	673	98.7	3992	10	MMU487852 Mus muscu
4	673	98.7	4294	10	AK122575 Mus muscu

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	661	96.9	2697	6	AX268596	AX268596 Sequence
6	661	96.9	2697	10	RNU87305	U87305 Rattus norv
7	661	96.9	3014	6	BD057524	BD057524 Netrin re
8	657.5	96.4	2784	6	CQ730306	CQ730306 Sequence
9	622.5	91.3	2881	6	AX527916	AX527916 Sequence
10	539	79.0	2270	9	BC041156	BC041156 Homo sapi
11	539	79.0	2612	6	CQ881064	CQ881064 Sequence
12	539	79.0	2780	6	CQ881054	CQ881054 Sequence
13	539	79.0	2986	6	CQ881052	CQ881052 Sequence
14	539	79.0	3646	6	CQ881060	CQ881060 Sequence
15	539	79.0	3646	9	AF055534	AF055534 Homo sapi
16	535	78.4	121282	9	AC027318	AC027318 Homo sapi
c 17	535	78.4	166534	2	AC034209	AC034209 Homo sapi
c 18	535	78.4	168168	2	AC012283	AC012283 Homo sapi
19	534	78.3	2962	5	AY187310	AY187310 Gallus ga
c 20	531.5	77.9	242128	2	AC123700	AC123700 Mus muscu
21	531	77.9	9299	10	MMU72634	MMU72634 Mus musculu
22	526	77.1	9328	10	AB118026	AB118026 Rattus no
23	523	76.7	2860	6	AX686445	AX686445 Sequence
24	523	76.7	2860	6	AX686447	AX686447 Sequence
25	523	76.7	2895	6	AX512281	AX512281 Sequence
26	523	76.7	2995	6	AX497288	AX497288 Sequence
27	523	76.7	3770	9	AY126437	AY126437 Homo sapi
28	523	76.7	3884	6	AX528525	AX528525 Sequence
29	523	76.7	3884	6	AX464012	AX464012 Sequence
30	523	76.7	3884	9	AY358351	AY358351 Homo sapi
31	523	76.7	3933	6	CQ850929	CQ850929 Sequence
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34	522	76.5	2831	6	BD057526	BD057526 Netrin re
35	522	76.5	2838	10	RNU87306	RNU87306 Rattus norv
36	522	76.5	3672	10	BC048162	BC048162 Mus muscu
37	522	76.5	3672	10	BC057560	BC057560 Mus muscu
38	522	76.5	3788	10	MMU487853	MMU487853 Mus muscu
c 39	511	74.9	231407	2	AC139592	AC139592 Rattus no
40	507	74.3	1482	5	AY764274	AY764274 Danio rer
41	502	73.6	2832	5	AY099459	AY099459 Xenopus l
42	488	71.6	4330	5	AY744919	AY744919 Petromyzo
43	485	71.1	2585	6	CQ842137	CQ842137 Sequence
44	485	71.1	2585	9	AK122615	AK122615 Homo sapi
45	485	71.1	2661	6	AX800717	AX800717 Sequence

ALIGNMENTS

RESULT 1	AX451652	Sequence 1 from Patent WO0233080.	2697 bp	DNA	linear	PAT 03-JUL-2002
LOCUS	AX451652	Sequence 1 from Patent WO0233080.				
DEFINITION	AX451652					
ACCESSION	AX451652					
VERSION	AX451652.1	GI:21698587				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1	Koehler,R.H.				
AUTHORS		Regulation of human netrin binding membrane receptor unc5h-1				
TITLE		Patent: WO 0233080-A 1 25-APR-2002;				
JOURNAL		Bayer Aktiengesellschaft (DE)				
FEATURES		Location/Qualifiers				
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		/mol_type="unassigned DNA"				
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ORIGIN	Alignment Scores:					
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	Score:	682.00	Matches:	117		
	Percent Similarity:	100.00%	Conservative:	0		
	Best Local Similarity:	100.00%	Mismatches:	0		

Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-10-624-932C-2_COPY_232_348 (1-117) x AX451652 (1-2697)			
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QY	21	SerValCysSerAlaSerCysGlyArgGlyTrrpGlnLysArgSerArgSerCysThrAsn	40
Db	754	TCGCTCTGACGGCCAGCTGTGGCGCGCTGGCAGAAACGAGCGGAGCTGCACCAAC	813
QY	41	ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys	60
Db	814	CCGGCGCTCTCAACCGGGCGCTTCTGTGAGGGGCGAGATGTCCAGAAACAGCCCTGC	873
QY	61	AlaThrLeuCysProValAspGlySerTrrpSerProTrrpSerLysTrrpSerAlaCysGly	80
Db	874	GCCACCTGTGCCAGTGGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTGGCTGTGGG	933
QY	81	LeuAspCysThrHisTrrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly	100
Db	934	CTGGACTGCACCCACTGGCGGAGCGTGGAGTGTCTGACCCAGCACCCCGCAACGGAGG	993
QY	101	GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu	117
Db	994	GAGGAGTGGCAGGGCACTGACCTGGACACCCGCAACTGTACCACTGACCTC	1044
RESULT 2			
LOCUS	AX449572	2752 bp	DNA linear PAT 03-JUL-2002
DEFINITION	Sequence 1 from Patent WO0210216.		
ACCESSION	AX449572		
VERSION	AX449572.1 GI:21698195		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Padigaru, M., Mezes, P., Mishra, V., Burgess, C., Casman, S., Grosse, W. M., Alsbrook, J. P., Lepley, D. M., Gerlach, V. L., Macdougall, J. R. and Smithson, G. Proteins and nucleic acids encoding same Patent: WO 0210216-A 1 07-FEB-2002; Curagen Corporation (US)		
FEATURES	Location/Qualifiers		
source	1..2752		
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	/mol_type="unassigned DNA"		
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ORIGIN			
Alignment Scores:	5.84e-36	Length:	2752
Pred. No.:	682.00	Matches:	117
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:	6		
US-10-624-932C-2_COPY_232_348 (1-117) x AX449572 (1-2752)			
QY	1	SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTrrpSerThrTrrThrGluTrrp	20
Db	739	AGCGCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGTGGTGCACGTGACCGAGTGG	798
QY	21	SerValCysSerAlaSerCysGlyArgGlyTrrpGlnLysArgSerArgSerCysThrAsn	40
Db	799	TCGCTCTGACGGCCAGCTGTGGCGCGCTGGCAGAAACGAGCGGAGCTGCACCAAC	858
QY	41	ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys	60
Db			
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Score: 673.00 Matches: 115
Percent Similarity: 99.15% Conservativity: 1
Best Local Similarity: 98.29% Mismatches: 1
Query Match: 98.68% Indels: 0
DB: 10 Gaps: 0

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Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrrGlnLysArgSerArgSerCysThrAsn 40
Db 985 TCCGCTCTCAGTCCAGCTGTGGCGTGGTGGCAGAAACGAGCGCGAGTGCACCAAC 1044

Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThraLys 60
Db 1045 CCGGCACCTCTCAACGGGGCGCCCTCTGTGAGGGGCAGATGTCCAGAAACAGCCCTGC 1104

Qy 61 AlaThrLeuCysProValAspGlySerTrrPsrProTrrPsrLysTrrPsrSerAlaCysGly 80
Db 1105 GCCACTCTGTGCCAGTGGAGCTGGAGCCCATGGAGTAAGTGTGAGCTGCGGG 1164

Qy 81 LeuAspCysThrHisTrrPsrArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 1165 CTTGACTGCACCCACTGGCGGAGCGGAGTGTCCGACCCAGCGCCCGCAACGAGGT 1224

Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1225 GAGGAGTCCCGGGTGTGACTGGACACCCGCAACTGTACAGTGACCTC 1275

RESULT 4
AK122575 4294 bp mRNA linear ROD 15-MAR-2003
LOCUS Mus musculus mRNA for mKIAA1976 protein.
DEFINITION AK122575
ACCESSION AK122575.1 GI:28972881
VERSION FLI CDNA.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
1 Okazaki,N., Kikuno,R., Ohara,O., Nagase,T., Ohara,O. and Koga,H.
Nakajima,D., Nagase,T., Ohara,O. and Koga,H.
Prediction of the coding sequences of mouse homologues of KIAA
gene: II. The complete nucleotide sequences of 400 mouse
KIAA-homologous cDNAs identified by screening of terminal sequences
of cDNA clones randomly sampled from size-fractionated libraries
DNA Res. 10, 35-48 (2003)
2 (bases 1 to 4294)
Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.
Direct Submission
Submitted (07-FEB-2003) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)
The CREATE program supported by Japan science and technology
corporation; cDNA full insert sequencing: Kazusa DNA Research
Institute; cDNA library construction, clone selection and 5'- &
3'-end one pass sequencing.
Location/Qualifiers
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note="vector:modified pbc SK+"
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gene

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PRQDPSPKLEQLQGLQIQEPRVLFHDSYHNLRLSHDVSSLWSKLLYSYQE
IPFHIWNGTQQYLHCTFTUERNASTDLSKQVWQVGGGSGFNINFTIKDTRF
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ORIGIN
Alignment Scores: 3.62e-35 Length: 4294
Pred. No.: 673.00 Matches: 115
Score: 673.00
Percent Similarity: 99.15% Conservativity: 1
Best Local Similarity: 98.29% Mismatches: 1
Query Match: 98.68% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x AK122575 (1-4294)

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Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrrGlnLysArgSerArgSerCysThrAsn 40
Db 752 TCCGCTCTGCGCGCGAGCTGTGGCGTGGTGGCAGAAACGAGCGCGAGTGCACCAAC 811

Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThraLys 60
Db 812 CCGGCACCTCTCAACGGGGCGCCCTCTGTGAGGGGCAGATGTCCAGAAACAGCCCTGC 871

Qy 61 AlaThrLeuCysProValAspGlySerTrrPsrProTrrPsrLysTrrPsrSerAlaCysGly 80
Db 872 GCCACTCTGTGCCAGTGGATGGAGCTGGAGCCCATGGAGTAAGTGTGAGCTGCGGG 931

Qy 81 LeuAspCysThrHisTrrPsrArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 932 CTTGACTGCACCCACTGGCGGAGCGGAGTGTCCGACCCAGCGCCCGCAACGAGGT 991

Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 992 GAGGAGTCCCGGGTGTGACTGGACACCCGCAACTGTACAGTGACCTC 1042

RESULT 5
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LOCUS AX268596
DEFINITION Sequence 15 from Patent WO0175440.
ACCESSION AX268596
VERSION AX268596.1 GI:16541710
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE
1 Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and
Pratt,J.Y.
Schizophrenia related genes
Patent: WO 0175440-A 15 11-OCT-2001;
WELFIDE CORPORATION (JP)
Location/Qualifiers
1. 2597
/organism="Rattus sp."
/mol_type="unassigned DNA"
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Alignment Scores:
Pred. No.: 1.38e-34 Length: 2697
Score: 661.00 Matches: 113
Percent Similarity: 97.44% Conservative: 1
Best Local Similarity: 96.58% Mismatches: 3
Query Match: 96.92% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x AX268596 (1-2697)
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Db 694 AGCACCTCTGACGGGTCATTGTTATGTGAACGGTGGTGGTGCAGCTGGACTGAGTGG 753

Qy 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAsn 40
Db 754 TCCGCTCTGCAGCCAGCTGTGGCGTGGAGTTCGTGGAGTAAGTGGTCAAGCTGTGGG 933

Qy 81 LeuAspCysThrHisTyrArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 934 CTTGACTGCACCCACTGGCGAGCGCGAGTGTCTTGACCCAGCACCCCGCCGATGGAGGT 993

Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 994 GAGGAGTGTGGGGTGTCTGACCTGGACACCCGCAACTGTACCACTGACCTC 1044

RESULT 6
RN087305
LOCUS RN087305 2697 bp mRNA linear ROD 15-MAY-1997
DEFINITION Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds.
ACCESSION U87305
VERSION U87305.1 GI:2055391
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 2697)
AUTHORS Leonardo,E.D., Hinck,L., Masu,M., Keino-Masu,K., Ackerman,S.L. and Tessier-Lavigne,M.
TITLE Vertebrate homologues of C. elegans UNC-5 are candidate netrin receptors
JOURNAL Nature 386 (6627), 833-838 (1997)
MEDLINE 97271897
PUBMED 9126742
REFERENCE 2 (bases 1 to 2697)
AUTHORS Leonardo,E.D., Hinck,L., Masu,M., Keino-Masu,K. and Tessier-Lavigne,M.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus, San Francisco, CA 94143-0452, USA
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location/Qualifiers
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/dev_stages="18 day embryo and 13 day embryo"
1..2697
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CDS
ORIGIN
Alignment Scores:
Pred. No.: 1.38e-34 Length: 2697
Score: 661.00 Matches: 113
Percent Similarity: 97.44% Conservative: 1
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US-10-624-932C-2_COPY_232_348 (1-117) x RN087305 (1-2697)
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Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
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Qy 81 LeuAspCysThrHisTyrArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 934 CTTGACTGCACCCACTGGCGAGCGCGAGTGTCTTGACCCAGCACCCCGCCGATGGAGGT 993

Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 994 GAGGAGTGTGGGGTGTCTGACCTGGACACCCGCAACTGTACCACTGACCTC 1044

RESULT 7
RN087524
LOCUS RN087524 3014 bp DNA linear PAT 27-AUG-2002
DEFINITION Netrin receptors.
ACCESSION RN087524
VERSION BD057524.1 GI:22603130
KEYWORDS JP 2001505062-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 3014)
AUTHORS Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.
TITLE Netrin receptors
JOURNAL Patent: JP 2001505062-A 1 17-APR-2001; THE REGENTS OF THE UNIV OF CALIFORNIA
COMMENT PN JP 2001505062-A/1
PD 17-APR-2001
PR 19-FEB-1998 JP 1998536840
PR 19-FEB-1997 US 08/808982
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PI MARC TESSIER LAVIGNE, DAVID E LEONARDO, LINDSAY HINCK, MASAYUKI
PI MASU,
PI KAZUKO KEINO MASU
PC C07K17/00, C07K17/00, C07K17/00, C07H21/02, C07H21/04, G01N33/53 CC
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FH Key Location/Qualifiers.
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FEATURES
Source

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Mismatches:	3
Indels:	0
Gaps:	0

US-10-624-932C-2 COPY 232 348 (1-117) x BD057524 (1-3014)

[illegible]

RESULT 8
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 LOCUS 2784 bp DNA linear PAT 03-FEB-2004
 DEFINITION Sequence 16240 from Patent WO02068579.
 CQ730306
 ACCESSION
 CQ730306.1 GI:42303801
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Venter, C.J., Adams M.C., Li, P.W. and Myers, E.W.
 Kits, such as nucleic acid arrays, comprising a majority of
 humanexons or transcripts, for detecting expression and other uses
 thereof
 PATENT: WO 02068579-A 16240 06-SEP-2002;
 PE Corporation (NY) (US)
 LOCATION/Qualifiers
 1. .2784
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 JOURNAL
 FEATURES
 source
 ORIGIN

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QY	10	-----	-----ValAsn 11
DB	754	GGCAGCTCGGTGCCCTGGCAGTGACATGTGGCTGTCTTCTGTCCGGCCAGTGAAC	813
QY	12	GlyGlyTrrSerThrTrrGluTrrSerValCysSerAlaSerCysGlyArgGlyTrr	31
DB	814	GTTGGGTGTTCGACGTGGACCGAGTGTCCGTCTGCAGCGCCAGCTGTGGGGCGGCTGG	873
QY	32	GlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGlu	51
DB	874	CAGAAACGAGCGCGAGCTGCACCAACCCGGCGCTCTCAACGGGGGCGCTTCTGTGTAG	933
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QY	72	ProTrrSerLysTrrSerAlaCysGlyLeuAspCysThrHisTrrArgSerArgGluCys	91
DB	994	CGCTGGAGCAAGTGTGTGGCTGTGGCTGGAGCTGACCCACTGTGGCGGAGCCGTGAGTGC	1053
QY	92	SerAspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeuAspThrArg	111
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QY	112	AsnCysThrSerAspLeu 117	
DB	1114	AACTGTACCAGTGACCTC 1131	
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VERSION	AX527916.1	GI:25172359	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Herrmann, J.L., Rastelli, L. and Shimkets, R.A.		
JOURNAL	Novel proteins and nucleic acids encoding same and antibodies directed against these proteins		
FEATURES	Patent: WO 0229038-A 1 11-APR-2002;		
source	Curegen Corporation (US)		
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QY 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
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QY 101 GluGluCysGlnGlyThrAaspLeuAaspThrArgAenCysThrSerAaspLeu 117
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DEFINITION Sequence 13 from Patent WO2004083371.
ACCESSION CQ881064
VERSION CQ881064.1 GI:54034173
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dahl, N.
TITLE Genes associated with obesity and methods for using the same
JOURNAL Patent: WO 2004083371-A 13 30-SEP-2004;
Astrazeneca AB (SE)

FEATURES
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Location/Qualifiers
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QY 81 LeuAaspCysThrHisTrrArgSerArgGluCysSerAaspProAlaProArgAenGlyGly 100
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QY 101 GluGluCysGlnGlyThrAaspLeuAaspThrArgAenCysThrSerAaspLeu 117
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RESULT 12
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DEFINITION Sequence 3 from Patent WO2004083371.
ACCESSION CQ881054
VERSION CQ881054.1 GI:54034167
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dahl, N.
TITLE Genes associated with obesity and methods for using the same
JOURNAL Patent: WO 2004083371-A 3 30-SEP-2004;
Astrazeneca AB (SE)

FEATURES
source
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Location/Qualifiers
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Query Match: 79.03% Indels: 0
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US-10-624-932c-2_COPY_232_348 (1-117) x CQ881054 (1-2780)

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QY 21 SerValCysSerAlaSerCysGlyArgGlyTrrGlnLysArgSerArgSerCysThrAen 40
Db 919 TCTGTGTGTAAACAGCGCGCTGTGGACGAGGTATCAGAAACGTACAAAGACCTGTACCAAC 978

QY 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
Db 979 CCGGCACCACTCAATGGGGGTCCTTCTGTGAAGGCGACAGTGTGCAGAAATAGCCCTGT 1038

QY 61 AlaThrLeuCysProValAaspGlySerTrrSerProTrrSerTrrSerAlaCysGly 80
Db 1039 ACTAGTGTATGCCAGTGGATGGCAGGTGGACGCCATGGACCAAGTGTCTACTTGTGGA 1098

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Db 1099 ACTGAGTGCACCACTGGCGCAGGAGGAGTGCACGGCCAGCCCCCAAGAAATGAGGC 1158

QY 101 GluGluCysGlnGlyThrAaspLeuAaspThrArgAenCysThrSerAaspLeu 117
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RESULT 13
CQ881052
LOCUS CQ881052 2986 bp DNA linear PAT 11-OCT-2004
DEFINITION Sequence 1 from Patent WO2004083371.
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 20:54:46 ; Search time 605.088 Seconds
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Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	682	100.0	2752	12 ADH71617	Adh71617 Human gen

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8	657.5	96.4	2907	4 AAK52261	Aak52261 Human pol
9	622.5	91.3	993	12 ADH71611	Adh71611 Human gen
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37	523	76.7	3884	4 AAS21316	Aas21316 Human cDN
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ALIGNMENTS

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XX
AC ADH71619;
XX
DT 25-MAR-2004 (first entry)
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DE Human gene of the invention NOV21f SEQ ID NO:515.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
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PR 06-JUN-2002; 2002US-0386376P.

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DT	25-MAR-2004 (first entry)	
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KW	vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;	
KW	obesity; diabetes; infectious disease; metabolic syndrome X;	
KW	dyslipidaemia.	
OS	Homo sapiens.	
XX	WO2003102155-A2.	
XX	11-DEC-2003.	
XX	03-JUN-2003; 2003WO-US017430.	
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PR	17-JUL-2002; 2002US-0401628P.	
PR	06-AUG-2002; 2002US-0402156P.	
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PR	12-AUG-2002; 2002US-0402832P.	
PA	(CURA-) CURAGEN CORP.	
PI	Alaobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;	
PI	Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;	
PI	Ettentberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;	
PI	Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;	
PI	MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;	
PI	Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;	
PI	Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;	
PI	Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;	
XX	Zhong H;	
XX	WPI: 2004-081935/08.	
XX	P-PSDB; ADH71614.	
DR	New NOVX polypeptides and nucleic acid molecules useful for preventing or	
PT	treating NOVX-associated disorders, e.g. cancer, diabetes, infection or	
PT	obesity, and in chromosome mapping, tissue typing or pharmacogenomics.	
XX	Example 21; SEQ ID NO 509; 1880pp; English.	
PS	The invention relates to a novel isolated polypeptide (NOVX). A	
XX	polypeptide of the invention has cytostatic, immunomodulator,	
CC	neuroprotective, neurotropic, anorectic, antidiabetic, antimicrobial, and	
CC	antilipaeamic activity, and may have a use in gene therapy, and as a	
CC	vaccine. The polypeptides are encoded by NOVX polynucleotides comprising	
CC	any of the 303 fully defined nucleotide sequences given in the	
CC	specification. The polypeptide is useful in the manufacture of a	
CC	medicament for treating a syndrome associated with a human disease. The	
CC	polypeptide, polynucleotide and antibody are useful in diagnosing,	
CC	treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,	
CC	Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious	
CC	diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are	
CC	further used as hybridisation probes, in chromosome mapping, tissue	
CC	typing, preventive medicine, and pharmacogenomics. The present sequence	
CC	encodes a NOVX polypeptide of the invention.	
XX	Sequence 1009 BP; 195 A; 314 C; 336 G; 164 T; 0 U; 0 Other;	
SQ	Alignment Scores:	
XX	Pred. No.:	2,95e-39
XX		

```
US-10-624-932C-2_COPY_232_348 (1-117) x ADH71613 (1-1009)
Qy 1 SerAlaSerAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 629 AGCGCCCTCCGCTGTCATCGTCTAGCGTGAACGGTGGTGGTGCAGCGTGCAGCGAGTGG 688
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 689 TCCGCTCTGCAGCGCAGCTGTGGCGCGCGTGGCAGAAACGGAGCCGAGAGTGCACCAAC 748
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 749 CCGCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGCGAGATGTCAGAAACAGCCTGC 808
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 809 GCCACCCCTGTGCCAGTGGACGGCAGCTGGAGCCCGTGGAGCAAGTGTGCGCGCTGTGGG 868
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 869 CTGAGCTGCACCCACTGGCGAGCGGTGAGTGTCTGACCCAGCAGCCCGGCAACGAGGG 928
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 929 GAGGAGTGCCAGGCGACTGACCTGGACACCCGCAACTGTACCACTGACCTC 979

RESULT 3
ABK52891
ID ABK52891 standard; DNA; 2697 BP.
AC ABK52891;
XX
XX
XX 27-AUG-2002 (first entry)
DE Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.
XX
XX Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human;
KW neotropic; neuroprotective; cytosolic; antiparkinsonian;
KW cerebroprotective; cancer; central nervous system; CNS; stroke;
KW Parkinson's disease; multiple sclerosis; Alzheimer's disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..2697
XX FT /*tag= a
XX FT /product= "Netrin binding membrane receptor UNC5H-1"
XX
XX WO200233080-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-EP011891.
XX
XX 16-OCT-2000; 2000US-0240061P.
XX
XX (FARB ) BAYER AG.
XX
XX Koehler RH;
XX
XX WPI: 2002-463314/49.
XX
XX P-PSDB; AAU97899.
XX
XX Novel human netrin binding membrane receptor polypeptide and
XX polynucleotides for identifying modulating agents useful in treating
XX diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
XX Alzheimer's disease.
XX
XX Claim 1; Fig 1; 94pp; English.
XX
XX This invention relates to the DNA and protein sequences of a novel
XX purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC
CC
```

sequence of the invention is useful as a probe for detecting a nucleic acid encoding the UNC5H-1 protein in a biological sample. The sequences of the invention are useful to screen for agents which decrease the activity of the UNC5H-1 protein. The sequences are also useful for screening agents which regulate (modulate) the activity of the protein of the invention. A pharmaceutical composition containing the protein of the invention or a reagent that modulates the activity of the UNC5H-1 protein may be useful for treating a UNC5H-1 dysfunction related disease such as cancer or a central nervous system (CNS) disorders (e.g. Parkinson's disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion proteins comprising the UNC5H-1 protein are useful for generating antibodies and for in various assay systems, and the protein can be used as a bait protein in a two-hybrid assay or three-hybrid assay. The method of the invention is useful for detecting a coding sequence for the UNC5H-1 protein. The present sequence represents a DNA sequence encoding the human netrin binding membrane receptor UNC5H-1 protein of the invention

Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.28e-39	Length:	2697
Score:	682.00	Matches:	117
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-624-932C-2_COPY_232_348 (1-117) x ABK52891 (1-2697)

Qy	1	SerAlaSerAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp	20
Db	694	AGCGCCCTCCGCTGTCATCGTCTAGCTGAACGGTGGTGGTGCAGCGTGCAGCGAGTGG	753
Qy	21	SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn	40
Db	754	TCCGCTCTGCAGCGCAGCTGTGGCGCGCTGGCAGAAACGGAGCCGAGTGCACCAAC	813
Qy	41	ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys	60
Db	814	CCGCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGCGAGATGTCAGAAACAGCCTGC	873
Qy	61	AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly	80
Db	874	GCCACCCCTGTGCCAGTGGACGGCAGCTGGAGCCCGTGGAGCAAGTGTGCGCGCTGTGGG	933
Qy	81	LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly	100
Db	934	CTGAGCTGCACCCACTGGCGGAGCGGTGAGTGTCTGACCCAGCAGCCCGGCAACGAGGG	993
Qy	101	GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu	117
Db	994	GAGGAGTGCCAGGCGACTGACCTGGACACCCGCAACTGTACCACTGACCTC	1044

RESULT 4
ABK37922
ID ABK37922 standard; cDNA; 2752 BP.
XX
XX
XX AC ABK37922;
XX
XX 21-MAY-2002 (first entry)
XX
XX cDNA encoding Human protein NOV1.
XX
XX Human; NOVX; ss; gene; cardiomyopathy; atherosclerosis; diabetes;
KW cell signal processing disorder; metabolic disorder; obesity; infection;
KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
KW psychosis; neurological disorder; anxiety; schizophrenia;
KW manic depression; dementia; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome; gene therapy.


```
US-10-624-932C-2_COPY_232_348 (1-117) x AAV52940 (1-3014)
Qy 1 SerAlaSerAlaAlaValIleValTyValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 694 AGCACCTCTGCAGCGGTCAATTGTTATGTGAACGGTGGTGGTGCAGCTGAGTGG 753
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 754 TCCGTCGTGCAGCGCAGCTGTGGCGGTGGTGGCAGAAACGAGCCGAGCTGCACCAAC 813
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 814 CCGGCACCTCTCAACGGGGGCGCTTCTGTGAGGGGCGAATGTCAGAAACAGCCTGC 873
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerProTrpSerAlaCysGly 80
Db 874 GCCACTGTGCCAGTGGATGGAGCTGGAGTTCTGTGAGTAAGTGGTCAGCCTGTGGG 933
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 934 CTTGACTGCACCCACTGGCGAGCGCGAGTGCTCTGACCCAGCACCCCGCATGGAGGT 993
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 994 GAGGAGTGTGGGGTGTGCTGACCTGGACACCCGCAACTGTACCACTGACCTC 1044
RESULT 8
AAK52261
ID AAK52261 standard; cDNA; 2907 BP.
XX
AC AAK52261;
XX
DT 06-NOV-2001 (first entry)
XX
Human polynucleotide SEQ ID NO 806.
XX
Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
XX WO200157190-A2.
XX
PD 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX
XX 27-APR-2000; 2000US-00560875.
XX
XX 20-JUN-2000; 2000US-00598075.
XX
XX 19-JUL-2000; 2000US-00620325.
XX
XX 01-SEP-2000; 2000US-00654936.
XX
XX 15-SEP-2000; 2000US-00663561.
XX
XX 20-OCT-2000; 2000US-00693325.
XX
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
XX Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX
XX P-PSDB; AAM79128.
XX
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
XX
XX Claim 1; Page 2691-2694; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX
```

```
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 2907 BP; 552 A; 966 C; 881 G; 508 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.74e-37 Length: 2907
Score: 657.50 Matches: 117
Percent Similarity: 80.14% Conservative: 0
Best Local Similarity: 80.14% Mismatches: 0
Query Match: 96.41% Indels: 29
DB: 4 Gaps: 1

US-10-624-932C-2_COPY_232_348 (1-117) x AAK52261 (1-2907)
Qy 1 SerAlaSerAlaAlaValIleValTy----- 9
Db 817 AGCGCCTCCGCTGCTGTGTCATCGTGTGCGGCGCCCGGAGCTCCCTGGTCACAGGGAGA 876
Qy 10 -----Valasn 11
Db 877 GGCACTGCGGTGCCCCCTGGGCGAGTGACATGTGGCTGTCTCTGTCGCGCCAGTGAAC 936
Qy 12 GlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrp 31
Db 937 GGTGGGTGTGTGCGAGTGGTGGTGTGTCAGCGCCAGCTGTGGGCGCGGCTGG 996
Qy 32 GlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGlu 51
Db 997 CAGAAACGGAGCCGAGCTGCACCAACCCGCGCTCTCAACGGGGCGCTTCTGTGTAG 1056
Qy 52 GlyGlnAsnValGlnLysThrAlaCysAlaThrLeuCysProValAspGlySerTrpSer 71
Db 1057 GGGCAGAAATGTCCAGAAACAGAGCTGCCACCTGTGCCAGTGGAGCGGAGCTGGAGC 1116
Qy 72 ProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSerArgGluCys 91
Db 1117 CCGTGGAGCAAGTGTGCGGCTGTGGGCTGGACTGCAACCCACCTGGCGGAGCCGTGAGTGC 1176
Qy 92 SerAspProAlaProArgAsnGlyGlyGluCysGlnGlyThrAspLeuAspThrArg 111
Db 1177 TCTGACCCAGACACCCCGCAACGGAGGGGAGAGTGGCCAGGGCACTGACCTGGACACCGC 1236
Qy 112 AsnCysThrSerAspLeu 117
Db 1237 AACTGTACCAAGTGACCTC 1254

RESULT 9
ADH71611
ID ADH71611 standard; DNA; 993 BP.
XX
AC ADH71611;
XX
DT 25-MAR-2004 (first entry)
XX
XX Human gene of the invention NOV21b SEQ ID NO:507.
XX
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia.
XX
```


CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

XX
SQ Sequence 2880 BP; 527 A; 984 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.36e-34 Length: 2880
Score: 622.50 Matches: 109
Percent Similarity: 94.07% Conservative: 2
Best Local Similarity: 92.37% Mismatches: 6
Query Match: 91.28% Indels: 1
DB: 12 Gaps: 1

US-10-624-932C-2_COPY_232_348 (1-117) x ADH71633 (1-2880)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAenGlyGlyTyrSerThrTrrpGluTrrp 20
Db 779 AGCGCTCCGCTGCTGCTATGCTACGTGAACGGTGGTGTGACGTGGACCGAGTGG 838
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrrpGlnLysArgSerArgSerCysThrAsn 40
Db 839 TCCGCTCTCAGCGCCAGCTGTGGCGCGCTGGCAGAAACGGAGCCGGAGCTGCACCAAC 898
Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenVal---GlnLysThrAla 59
Db 899 CCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGCGAGATGTCCATGACCGCACCGTC 958
Qy 60 CysAlaThrLeuCysProValAspGlySerTrrpSerProTrrpSerLysTrrpSerAlaCys 79
Db 959 TCCTCTGCTGTCTCTGTGAGCGGAGCTGGAGCCCGGTGAGCAAGTGTGGCCCTGT 1018
Qy 80 GlyLeuAspCysThrHisTrrpArgSerArgGlyCysSerAspProAlaProArgAsnGly 99
Db 1019 GGGCTGGACTGCACCCACTGGCGGAGCGTGTGAGTCTCTGACCCAGCACCCCGCAACGGA 1078
Qy 100 GlyGluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1079 GGGGAGGAGTGCCAGGGCACTGACCTGGACACCCCGCAACTGTACCACTGACCTC 1132

RESULT 11

ABK49422
ID ABK49422 standard; DNA; 2881 BP.

XX
AC ABK49422;

XX
DT 15-JUL-2002 (first entry)

XX
DE DNA encoding human UNC5-like protein NOV1.

XX
KW Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;
KW cell signal processing; metabolic pathway modulation; cancerous tissue;
KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;
KW chromosome 13; gene; ds.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
CDS 87..2786
FT /tag= a
FT /product= "Human UNC5-like protein NOV1"

XX
FN WO200229038-A2.

XX
PD 11-APR-2002.

XX
FF 04-OCT-2001; 2001WO-US031377.

XX
PR 04-OCT-2000; 2000US-0237862P.

XX
PA (CURA-) CURAGEN CORP.

XX
PI Herrmann JL, Rastelli L, Shinkets RA;

XX
DR WPI; 2002-340104/37.

XX
P-PSDB; AAU79939.

PT Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for
PT treating cardiomyopathy, atherosclerosis, and cancer.

XX
PS Claim 8; Page 7-8; 180pp; English.

XX
CC The present invention relates to a new NOVX polypeptide having a 900
CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)
CC residue amino acid sequence, as given in the specification. The novel
CC polypeptide, and its encoding polynucleotide, are used to treat
CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell
CC signal processing and metabolic pathway modulation, in a human. Detecting
CC the polypeptide or polynucleotide is useful for identifying cancerous
CC tissue. The antibody can be used to treat diabetes or cancer. The host
CC cells can be used to produce non-human transgenic animals useful in drug
CC screening. The present nucleic acid sequence is that of the human UNC5-
CC like NOV1 gene located on chromosome 13. This sequence encodes the human
CC UNC5-like protein NOV1 of the invention

SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.36e-34 Length: 2881
Score: 622.50 Matches: 109
Percent Similarity: 94.07% Conservative: 2
Best Local Similarity: 92.37% Mismatches: 6
Query Match: 91.28% Indels: 1
DB: 6 Gaps: 1

US-10-624-932C-2_COPY_232_348 (1-117) x ABK49422 (1-2881)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAenGlyGlyTrrpSerThrTrrpGluTrrp 20

Db 780 AGCGCTCCGCTGCTGCTATGCTACGTGAACGGTGGTGTGACGTGGACCGAGTGG 839

Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrrpGlnLysArgSerArgSerCysThrAsn 40

Db 840 TCCGCTCTCAGCGCCAGCTGTGGCGCGCTGGCAGAAACGGAGCCGGAGCTGCACCAAC 899

Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenVal---GlnLysThrAla 59

Db 900 CCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGCGAGATGTCCATGACCGCACCGTC 959

Qy 60 CysAlaThrLeuCysProValAspGlySerTrrpSerProTrrpSerLysTrrpSerAlaCys 79

Db 960 TCCTCTGCTGTCTCTGTGAGCGGAGCTGGAGCCCGGTGAGCAAGTGTGGCCCTGT 1019

Qy 80 GlyLeuAspCysThrHisTrrpArgSerArgGlyCysSerAspProAlaProArgAsnGly 99

Db 1020 GGGCTGGACTGCACCCACTGGCGGAGCGTGTGAGTCTCTGACCCAGCACCCCGCAACGGA 1079

Qy 100 GlyGluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117

Db 1080 GGGGAGGAGTGCCAGGGCACTGACCTGGACACCCCGCAACTGTACCACTGACCTC 1133

RESULT 12

ADH71649
ID ADH71649 standard; DNA; 2881 BP.

XX
AC ADH71649;

XX
DT 25-MAR-2004 (first entry)

XX
DE Human gene of the invention NOV21u SEQ ID NO:545.

XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.


```
QY 60 CysAlaThrLeuCyProValaspGlySerTrpSerProTrpSerLysTrpSerAlaCys 79
   :::
Db 960 TCCTCTCTGCTGTCTGTGGACGGCAGCTGGAGCCCGTGGAGCAAGTGTGGCCCTGT 1019

QY 80 GlyLeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAnGly 99
   |||||
Db 1020 GGGCTGGACTGCACCCACTGGCGGAGCGGTGAGTGTCTCTGACCCAGCACCCCGCAACGGA 1079

QY 100 GlyGluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
   |||||
Db 1080 GGGGAGGAGTGCCAGGGGCACTGACCTGGACACCCGCAACTGTACCACTGACCTC 1133

RESULT 13
ADH71635
ID ADH71635 standard; DNA; 2881 BP.
XX
AC ADH71635;
XX
DT 25-MAR-2004 (first entry)
XX
DB Human gene of the invention NOV21n SEQ ID NO:531.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
FN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PP 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
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PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
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PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
PA Alsobrook JP, Alvarez E, Anderson DW, Boldog PL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacIachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shency SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71636.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 531; 1880pp; English.
PS
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaeamic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing. The
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
```


CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

XX
SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.36e-34 Length: 2881
Score: 622.50 Matches: 109
Percent Similarity: 94.07% Conservative: 2
Best Local Similarity: 92.37% Mismatches: 6
Query Match: 91.28% Indels: 1
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Db 900 CCGCGCGCTCTCAACGGGGGCGCTTCTGTGAGGGGCGAGATGTCATGACCGACCGTC 959
Qy 60 CysAlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCys 79
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Db 1020 GGGCTGGACTGCACCCACTGGCGAGCGCTGAGTGTCTGTACCCAGCAGCCCGCAACGGA 1079
Qy 100 GlyGluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1080 GGGAGGAGTGCCAGGGCAGTGCACCTGGACACCCGCACTGTACAGTGACCTC 1133

RESULT 14

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XX
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AC ADH71637;
XX
XX 25-MAR-2004 (first entry)
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XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antipneumic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia.
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XX Homo sapiens.
XX
XX WO2003102155-A2.
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XX 11-DEC-2003.
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XX 03-JUN-2003; 2003WO-US017430.
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XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
XX 05-JUN-2002; 2002US-0386047P.
XX 06-JUN-2002; 2002US-0386376P.
XX 06-JUN-2002; 2002US-0386453P.
XX 06-JUN-2002; 2002US-0386864P.
XX 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
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PR 17-JUL-2002; 2002US-0396706P.
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PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
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PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
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PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798P.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.

(CURA-) CURAGEN CORP.

XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FR, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;

PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
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PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX WPI: 2004-081935/08.
DR P-PSDB; ADH71638.

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 21; SEQ ID NO 533; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A

CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

XX SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.36e-34 Length: 2881
Score: 622.50 Matches: 109
Percent Similarity: 94.07% Conservative: 2
Best Local Similarity: 92.37% Mismatches: 6
Query Match: 91.28% Indels: 1
DB: 12 Gaps: 1

US-10-624-932c-2_copy_232_348 (1-117) x ADH71637 (1-2881)

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Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
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RESULT 15

ADH71641

ID ADH71641 standard; DNA; 2881 BP.

XX

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XX 25-MAR-2004 (first entry)
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KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX Homo sapiens.
OS WO2003102155-A2.
XX 11-DEC-2003.
XX 03-JUN-2003; 2003WO-US017430.
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
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GenCore version 5.1.6
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Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%

Maximum Match 100%

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- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	539	79.0	3008	4	US-09-949-016-4794
4	522	76.5	2831	2	US-08-808-982-3
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6	290	42.5	114139	4	US-09-949-016-16536
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8	268	39.3	5749	4	US-09-262-537-48
9	266	39.0	5784	4	US-09-949-016-462
10	262	38.4	5722	4	US-09-657-472-1
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ALIGNMENTS

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; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/808,982
; APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:

Alignment Scores:
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Best Local Similarity: 73.50% Mismatches: 16
Query Match: 79.03% Indels: 0
DB: 4 Gaps: 0

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Qy 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAsn 40
Db 324 TCTGTGTGTAAACAGCGCTGTGGACAGGGTATCAGAAACGTACAAAGACTGTACCAAC 383

Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 384 CCGGCACCACTCAATGGGGGTCCTTCTGTGAAGGGCAGAGTGTGCAGAAATAGCCTGT 443

Qy 61 AlaThrLeuCysProValAspGlySerTyrSerProTyrSerLysTyrSerAlaCysGly 80
Db 444 ACTAGTATGCCCCAGTGGATGGCAGGTGGAGCCCATGGAGCAAGTGTCTACTTGTGGA 503

Qy 81 LeuAspCysThrHisTyrArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 504 ACTGAGTGACCCACTGGCGCAGGAGGAGTGCAGCGGCCCGCCCAAGATGGAGGC 563

Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 564 AAGGACTCGCAGCGGCTCGTCTTGCATCAAGAACTGCACTGATGGGCTT 614

RESULT 4

US-08-808-982-3
; Sequence 3, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid

STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-808-982-3

Alignment Scores:
Pred. No.: 1.92e-35 Length: 2831
Score: 522.00 Matches: 84
Percent Similarity: 82.05% Conservative: 12
Best Local Similarity: 71.79% Mismatches: 21
Query Match: 76.54% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x US-08-808-982-3 (1-2831)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAlaSerGlyTyrSerThrTyrThrGluTyr 20
Db 700 AGCAGCGGGCCAGTCATCTATGTGAACGGAGTTGGTCAGTGGCAGAAATGG 759

Qy 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAsn 40
Db 760 TCACCTGTCTTAACCGCTGCGCGGAGTTGGCAGAAACGTACTAGGACCTGCACCAAC 819

Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 820 CCAGCCCACTCAATGGAGGTGCCTTCTGCGAGGGACAGGCTTCCAGAACGCGCTTGC 879

Qy 61 AlaThrLeuCysProValAspGlySerTyrSerProTyrSerLysTyrSerAlaCysGly 80
Db 880 ACCACGTTGTGCCAGTGGATGGAGCGTGGACTGAGTGGAGCAAGTGTTCGCTTCGACG 939

Qy 81 LeuAspCysThrHisTyrArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 940 ACAGAGTGTGGCACTGGCGCAGCGCGAGTGCATGGCACCGCCCGCCAGAACGAGGC 999

Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1000 CGTGACTGCAGCGGACGCTACTTGACTCCAGAACTGCACCGATGGGCTG 1050

RESULT 5

US-09-306-902A-3
; Sequence 3, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341


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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 462
; LENGTH: 5784
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-462

Alignment Scores:
Pred. No.: 4,04e-13 Length: 5784
Score: 266.00 Matches: 47
Percent Similarity: 57.01% Conservative: 14
Best Local Similarity: 43.93% Mismatches: 42
Query Match: 39.00% Indels: 4
DB: Gaps: 2

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-949-016-462 (1-5784)

QY 11 AsnGlycTyrSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGly 30
   :::::::::::::::::::::::::::::|||||:|||||:|||||:|||||:|||||:
Db 1548 GACGGCGCGTGGAGCACCTGGTCACTTGGTCTTTCATGCTGTGACCTGTGGAGTTGC 1607
   :::::::::::::::::::::::::::::|||||:|||||:|||||:|||||:|||||:

QY 31 TrpGlnlyeArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCys 50
   :::::::::::::::::::::|||||:|||||:|||||:|||||:|||||:
Db 1608 AATATCACAGCATCGTCTCTGCAACTCCCCAGTCCCCAGATGGGGGGCAAGATTGC 1667
   :::::::::::::::::::::|||||:|||||:|||||:|||||:|||||:

QY 51 GluGlyGlnAsnValGlnlyThrAlaCys---AlaThrLeuCysProValAspGlySer 69
   :::::::::::::::::::::|||||:|||||:|||||:|||||:|||||:
Db 1668 AAAGGGAGTGGCGGGAGACCAAGCGCTGCCAGGGCGGCCCATGCCAATCGATGCCCGC 1727
   :::::::::::::::::::::|||||:|||||:|||||:|||||:|||||:

QY 70 TrpSerProTrpSerlystTrpSerAlaCysGlyLeuAspCysThr-----HisTrp 86
   :::::::::::::::::::::|||||:|||||:|||||:|||||:|||||:
Db 1728 TGGAGCCCGCTGGTCCCGCTGGTGGCGCTGCACCTGTGCACCTGTGCGGATCCGGAG 1787
   :::::::::::::::::::::|||||:|||||:|||||:|||||:|||||:

QY 87 ArgSerArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThr 106
   :::::::::::::::::::::|||||:|||||:|||||:|||||:|||||:
Db 1788 CGACCCGGGTGCAACAGCCCTGAGCCTCAGTACGGAGGAGGCCCTCGCTGGGGGAT 1847
   :::::::::::::::::::::|||||:|||||:|||||:|||||:|||||:

QY 107 AspLeuAspThrArgAsnCys 113
   :::::::::::::::::::::|||||:|||||:|||||:|||||:|||||:
Db 1848 GTCCAGGAGCGTCAGATGTGC 1868
   :::::::::::::::::::::|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-09-657-472-1
; Sequence 1, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5722
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-09-657-472-1

Alignment Scores:
Pred. No.:      8.77e-13      Length:      5722
Score:          262.00      Matches:      45
Percent Similarity: 57.94%      Conservative: 17
Best Local Similarity: 42.06%      Mismatches: 41
Query Match:      38.42%      Indels:      4
DB:              4          Gaps:      2

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-657-472-1 (1-5722)

Qy  11 AsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGly 30
    ::::::::::::::::::::
Db  1414 GATGGTGGCTGGAGCCACTGGTCCCGGGTCATCTTGTTCGTGACATGGGTGATGGT 1473
    ::::::::::::::::::::

Qy  31 TrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCys 50
    ::::::::::::::::::::
Db  1474 GTGATCAAGATCCGGCTCTGCAACTCTCCAGCCCCCAGATGGAATGGGAACCTGT 1533
    ::::::::::::::::::::

Qy  51 GluGlyGlnAsnValGlnLysThrAlaCys---AlaThrLeuCysProValAspGlySer 69
    ::::::::::::::::::::
Db  1534 GAAGCGAAGCGCGGAGACCAAGACCTGCAGAAAGAGCGCTGCCCCCATCAATGGAGGC 1593
    ::::::::::::::::::::

Qy  70 TrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCys-----ThrHisTrp 86
    ::::::::::::::::::::
Db  1594 TGGGGTCTTGGTCACCATGGAGCATCTGTCTGTCACCTGGAGGAGGGGTACAGAAA 1653
    ::::::::::::::::::::

Qy  87 ArgSerArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThr 106
    ::::::::::::::::::::
Db  1654 CGTAGTCGTCTCTGCAACAACCCCGCACCCAGTTTGGAGGCAAGGACTGGTTGGTGAT 1713
    ::::::::::::::::::::

Qy  107 AspLeuAspThrArgAsnCys 113
    ::::::::::
Db  1714 GTAACAGAAACACAGATCTGC 1734

RESULT 11
US-09-854-845-15
; Sequence 15, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054e1 Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2820
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-15

Alignment Scores:
Pred. No.:      4.01e-13      Length:      2820
Score:          261.50      Matches:      50
Percent Similarity: 56.19%      Conservative: 9
Best Local Similarity: 47.62%      Mismatches: 41
Query Match:      38.34%      Indels:      5
DB:              4          Gaps:      3

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-854-845-15 (1-2820)

Qy  10 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 29
    ::::::::::::::::::::
```

```
Db  2134 GTTCGGGGTGTGGTCTCTGCTGGACCTCATGGTCTCCATGCTCAGCTTCTCTGTGGTGG 2193
    ::::::::::::::::::::

Qy  30 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 49
    ::::::::::::::::::::
Db  2194 GGTCACTATCAACGACACCCGTTCTTCGACACGAGCCCGCCCTCCCGAGGTGAGGACATC 2253
    ::::::::::::::::::::

Qy  50 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThr---LeuCysProValAspGly 68
    ::::::::::::::::::::
Db  2254 TGTCTCGGGCTGCACACGAGGAGGACATATGTGCCACACAGGCGCTGCCCA-----GAA 2307
    ::::::::::::::::::::

Qy  69 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 88
    ::::::::::::::::::::
Db  2308 GGCTGGTGGCCCTGGTCTGAGTGGAGTAAGTGCACTGACGACGAGCCGAGCGCGAAGC 2367
    ::::::::::::::::::::

Qy  89 ArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeu 108
    ::::::::::::::::::::
Db  2368 CGGCACCTGTGAGGAGCTCTCCCA-----GGGTCCAGCGCTGTGTGGAAACAGCAGC 2421
    ::::::::::::::::::::

Qy  109 AspThrArgAsnCys 113
    ::::::::::
Db  2422 CAGAGCGCCCGCTGC 2436

RESULT 12
US-09-854-845-13
; Sequence 13, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054e1 Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2865
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-13

Alignment Scores:
Pred. No.:      4.09e-13      Length:      2865
Score:          261.50      Matches:      50
Percent Similarity: 56.19%      Conservative: 9
Best Local Similarity: 47.62%      Mismatches: 41
Query Match:      38.34%      Indels:      5
DB:              4          Gaps:      3

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-854-845-13 (1-2865)

Qy  10 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 29
    ::::::::::::::::::::
Db  2134 GTTCGGGGTGTGGTCTCTGCTGGACCTCATGGTCTCCATGCTCAGCTTCTCTGTGGTGG 2193
    ::::::::::::::::::::

Qy  30 GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 49
    ::::::::::::::::::::
Db  2194 GGTCACTATCAACGACACCCGTTCTTCGACACGAGCCCGCCCTCCCGAGGTGAGGACATC 2253
    ::::::::::::::::::::

Qy  50 CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThr---LeuCysProValAspGly 68
    ::::::::::::::::::::
Db  2254 TGTCTCGGGCTGCACACGAGGAGGACATATGTGCCACACAGGCGCTGCCCA-----GAA 2307
    ::::::::::::::::::::

Qy  69 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 88
    ::::::::::::::::::::
Db  2308 GGCTGGTGGCCCTGGTCTGAGTGGAGTAAGTGCACTGACGACGAGCCGAGCGCGAAGC 2367
    ::::::::::::::::::::
```



```

; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3150
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-1

Alignment Scores:
Pred. No.: 4.6e-13 Length: 3150
Score: 261.50 Matches: 50
Percent Similarity: 56.19% Conservative: 9
Best Local Similarity: 47.62% Mismatches: 41
Query Match: 38.34% Indels: 5
DB: 4 Gaps: 3

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-854-845-1 (1-3150)

Qy 10 ValAsnGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArg 29
Db 2419 GTTCGGGGTGTCTGGTCTCTGCTGGACCTCATGGTCTCCATGCTCAGCTTCCTGTGGTGG 2478
Qy 30 GlyTrpGlnIysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe 49
Db 2479 GGTCACTATCAACGGACCCGCTCTCCACACCGCCGCCCTCCCTCCAGGTGAGGACATC 2538
Qy 50 CysGluGlyGlnAsnValGlnIysThrAlaCysAlaThr---LeuCysProValAspGly 68
Db 2539 TGTCTCGGGCTGCACCGAGGAGGCACCTATGTGCCACACAGGCGCTGCCCA-----GAA 2592
Qy 69 SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer 88
Db 2593 GGCTGTGTGGCCCTGGTCTGAGTGGAGTAGTAGTCACTGACGACGAGGCCAGAGCCGAAGC 2652
Qy 89 ArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeu 108
Db 2653 CGGCACTGTGAGGAGCTCCTCCCA-----GGGTCCAGGCGCTGTGCTGGAAACAGCAGC 2706
Qy 109 AspThrArgAsnCys 113
Db 2707 CAGAGCGCGCCCTGC 2721

RESULT 15
US-09-854-845-7
; Sequence 7, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 7
; LENGTH: 3237
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-7

Alignment Scores:
Pred. NO.: 4 76e-13 Length: 3237
Score: 261.50 Matches: 50
Percent Similarity: 56.19% Conservative: 9
Best Local Similarity: 47.62% Mismatches: 41
Query Match: 38.34% Indels: 5
DB: 4 Gaps: 3

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-854-845-7 (1-3237)

Qy	10	ValAsnGlyGlyTrpSerThrTrpGluTrpSerValCysSerAlaSerCysGlyArg	29
Db	2551	GTTCGGGTGCTTGGTCTCTGCTGGACCTCATGGTCTCCATGCTCAGCTTCCTGTGGTGGG	2610
Qy	30	GlyTrpGlnLysArgSerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPhe	49
Db	2611	GGTCACTATCAACGACACCCGTTCTTGACACCCCGCCCTCCCGAGGTGAGGACATC	2670
Qy	50	CysGluGlyGlnAsnValGlnLysThrAlaCysAlaThr---LeuCysProValAspGly	68
Db	2671	TGTCCTGGGCTGCACACGGAGGAGGACTATGTGCCACACAGGCTGCCCA-----GAA	2724
Qy	69	SerTrpSerProTrpSerLysTrpSerAlaCysGlyLeuAspCysThrHisTrpArgSer	88
Db	2725	GGCTGGTCCGCTGGTCTGAGTGGAGTAAGTGCACTGACGACGGAGCCGAGAGCGAAGC	2784
Qy	89	ArgGluCysSerAspProAlaProArgAsnGlyGlyGluGluCysGlnGlyThrAspLeu	108
Db	2785	CGGCACTGTGAGGAGCTCTCCCA-----GGGTCCAGCCCTGTGTGGAACACAGCAGC	2838
Qy	109	AspThrArgAsnCys	113
Db	2839	CAGAGCGCCCTGTC	2853

Search completed: September 9, 2005, 09:51:14
Job time : 208.494 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 9, 2005, 04:41:16 ; Search time 1167.56 Seconds
(without alignments)
658.098 Million cell updates/sec

Title: US-10-624-932C-2_COPY_232_348

Perfect score: 682

Sequence: 1 SASAAVIVYVNGWSTWET.....NGBECQGTDLDRNCTSDL 117

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161709_15882/app_query.fasta_1.1386
-DB=Published Applications NA -QWITS=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10624932 @CGN 1 1 989 @runat_08092005_161709_15882
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOC=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=10 -YGAPEXT=0.5 -DELOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	682	100.0	2752	10	US-09-918-779-1	Sequence 1, Appli
2	682	100.0	2752	18	US-10-624-932-1	Sequence 1, Appli
3	661	96.9	2697	16	US-10-240-154-15	Sequence 15, Appl
4	661	96.9	3014	10	US-09-933-461-1	Sequence 1, Appli
5	661	96.9	3014	14	US-10-256-702-1	Sequence 1, Appli
6	622.5	91.3	2881	10	US-09-970-944-1	Sequence 1, Appli
7	523	76.7	2860	17	US-10-087-684-1	Sequence 1, Appli
8	523	76.7	2860	17	US-10-087-684-3	Sequence 3, Appli
9	523	76.7	2860	17	US-10-218-779-1	Sequence 1, Appli
10	523	76.7	2860	17	US-10-218-779-3	Sequence 3, Appli
11	523	76.7	2895	18	US-10-037-417-37	Sequence 37, Appli
12	523	76.7	2995	11	US-09-972-211-55	Sequence 55, Appl
13	523	76.7	2995	18	US-10-096-625-55	Sequence 55, Appl
14	523	76.7	3485	9	US-09-816-828-18	Sequence 18, Appli
15	523	76.7	3501	17	US-10-295-027-1123	Sequence 1123, Ap
16	523	76.7	3884	14	US-10-028-072-145	Sequence 145, App
17	523	76.7	3884	14	US-10-140-808-145	Sequence 145, App
18	523	76.7	3884	14	US-10-121-049-145	Sequence 145, App
19	523	76.7	3884	14	US-10-123-904-145	Sequence 145, App
20	523	76.7	3884	14	US-10-140-470-145	Sequence 145, App
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22	523	76.7	3884	14	US-10-176-318-145	Sequence 145, App
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24	523	76.7	3884	14	US-10-137-865-145	Sequence 145, App
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28	523	76.7	3884	14	US-10-142-419-145	Sequence 145, App
29	523	76.7	3884	14	US-10-123-262-145	Sequence 145, App
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31	523	76.7	3884	14	US-10-121-050-145	Sequence 145, App
32	523	76.7	3884	14	US-10-141-755-145	Sequence 145, App
33	523	76.7	3884	14	US-10-143-032-145	Sequence 145, App
34	523	76.7	3884	14	US-10-123-108-145	Sequence 145, App
35	523	76.7	3884	14	US-10-123-236-145	Sequence 145, App
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37	523	76.7	3884	14	US-10-140-921-145	Sequence 145, App
38	523	76.7	3884	14	US-10-140-928-145	Sequence 145, App
39	523	76.7	3884	14	US-10-121-045-145	Sequence 145, App
40	523	76.7	3884	14	US-10-123-292-145	Sequence 145, App
41	523	76.7	3884	14	US-10-123-903-145	Sequence 145, App
42	523	76.7	3884	14	US-10-124-819-145	Sequence 145, App
43	523	76.7	3884	14	US-10-124-822-145	Sequence 145, App
44	523	76.7	3884	14	US-10-140-925-145	Sequence 145, App
45	523	76.7	3884	14	US-10-160-498-145	Sequence 145, App

ALIGNMENTS

RESULT 1
US-09-918-779-1
; Sequence 1, Application US/09918779
; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shinkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Sureeh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William

```
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennnda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-779-1
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Alignment Scores:
Pred. No.: 5.62e-60 Length: 2752
Score: 682.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-918-779-1 (1-2752)

Qy 1 SerAlaSerAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
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Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 799 TCCGTCTCAGCGCCAGCTGTGGGCGCGCTGGCAGAAACGGAGCCGGAGCTGCACCAAC 858

Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 859 CCGCGCGCTCTCAACGGGGGGCGCTTCTGTGAGGGGGCAGATGTCCAGAAACAGCCCTGC 918

Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
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Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 979 CTGGACTGCACCCACTGGCGGAGCGGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGG 1038
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Qy 101 GluCluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1039 GAGGAGTGCCAGGGCACTGACCTGGACACCGGCAACTGTACCACTGACCTC 1089

RESULT 2
US-10-624-932-1
; Sequence 1, Application US/10624932
; Publication No. US20040096877A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shinkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennnda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/10/624,932
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918,779
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-624-932-1

Alignment Scores:
Pred. No.: 5.62e-60 Length: 2752
Score: 682.00 Matches: 117
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x US-10-624-932-1 (1-2752)

Qy 1 SerAlaSerAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
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Db 739 AGCGCTCCGCTGCTGTATCTACGTGACCGTGGTGGTGTGACGTGACCGAGTGG 798
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Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
Db 859 CGCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGCGAGATGTCCAGAAACAGCCTGC 918
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 919 GCCACCTCTGCCCACTAGACGCGAGCTGGAGCCGCTGGAGCAAGTGGTCCGCTGTGGG 978
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAenGlyGly 100
Db 979 CTGGACTGCACCCACTGGCGGAGCGTGTGCTCTGACCCAGCACCCCGCAACGGAGGG 1038
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAenCysThrSerAspLeu 117
Db 1039 GAGGAGTCCAGGCGCACTGACTGGACACCCCGCAACCTGTACAGTGACCTC 1089

RESULT 3
; US-10-240-154-15
; Sequence 15, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240.154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 2697
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15
Alignment Scores:
Pred. No.: 7,81e-58 Length: 2697
Score: 661.00 Matches: 113
Percent Similarity: 97.44% Conservative: 1
Best Local Similarity: 96.58% Mismatches: 3
Query Match: 96.92% Indels: 0
DB: 16 Gaps: 0

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Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAen 40
Db 754 TCCGTCTGCAGCGCCAGCTGTGGGCGTGGCTGGCAGAAACCGAGCCGAGCTGCACCAAC 813
Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
Db 814 CGCGCACCTCTCAACGGGGCGCGCTTCTGTGAGGGGCGAGATGTCCAGAAACAGCCTGC 873
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 874 GCCACTCTGTGCCCACTGATGGAGCTGGAGTTCGTGGAGTAAAGTGGTCAAGCTGTGGG 933
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAenGlyGly 100
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Db 934 CTTGACTGCACCCACTGGCGGAGCCGAGTGTCTGACCCAGCACCCCGCAATGGAGGT 993
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAenCysThrSerAspLeu 117
Db 994 GAGGAGTGTGGGGTGTGACCTGGACACCCCGCACTGTGTACAGTGACCTC 1044

RESULT 4
; US-09-933-261-1
; Sequence 1, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-933-261-1

Alignment Scores:
Pred. No.: 8.77e-58 Length: 3014
Score: 661.00 Matches: 113
Percent Similarity: 97.44% Conservative: 1
Best Local Similarity: 96.58% Mismatches: 3
Query Match: 96.92% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x US-09-933-261-1 (1-3014)
Qy 1 SerAlaSerAlaAlaValIleValTyrValAenGlyGlyTrpSerThrTrpThrGluTrp 20
Db 694 AGCACCTCTGACGGGTCTATTGTATGTGAACGGTGGTGGTGCAGCTGCACTGAGTGG 753
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAen 40
Db 754 TCCGTCTGCAGCGCCAGCTGTGGGCGTGGCTGGCAGAAACCGAGCCGAGCTGCACCAAC 813
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Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
Db 814 CCGGACCTCTCAACGGGGGGCCCTTCTGTAGGGGGCAGAAATGTCAGAAACAGCCTGC 873
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 874 GCCACTCTGTGCCACGATGGATGGAGCTGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGG 933
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAenGlyGly 100
Db 934 CTTGACTGCACCCACTGGCGAGCGGAGTGTCTGACCCAGCAGCCCGCAATGGAGGT 993
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAenCysThrSerAspLeu 117
Db 994 GAGGAGTGTGGGGTGTGACCTGGACACCCGCAACTGTACCACTGACCTC 1044

RESULT 5
US-10-256-702-1
; Sequence 1, Application US/10256702
; Publication No. US20030059859A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Maeu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/256,702
; FILING DATE: 27-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-256-702-1
Alignment Scores:
Pred. No.: 8.77e-58 Length: 3014
Score: 661.00 Matches: 113
Percent Similarity: 97.44% Conservative: 1
Best Local Similarity: 96.58% Mismatches: 3
Query Match: 96.92% Indels: 0
DB: 14 Gaps: 0
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Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 694 AGCACCTCTCGACGGGTCAATTGTTATGTGAACGGTGGTGGTGCACGTCGACTGAGTGG 753
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 754 TCCGTCTGCAAGCCAGCTGTGGCGGTGGTGGCAGAAACGGAGCCGAGCTGCACCAAC 813
Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
Db 814 CCGGACCTCTCAACGGGGGGCGCTTCTGTGAGGGGCAGAAATGTCAGAAACAGCCTGC 873
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 874 GCCACTCTGTGCCAGTGGATGGAGCTGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGG 933
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAenGlyGly 100
Db 934 CTTGACTGCACCCACTGGCGAGCGGAGTGTCTGACCCAGCAGCCCGCAATGGAGGT 993
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAenCysThrSerAspLeu 117
Db 994 GAGGAGTGTGGGGTGTGACCTGGACACCCGCAACTGTACCACTGACCTC 1044

RESULT 6
US-09-970-944-1
; Sequence 1, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1e1 Proteins and Nucleic Acids Encoding Same an
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; CURRENT FILING DATE: 2002-05-02
; PRIOR FILING DATE: 60/237,862
; APPLICATION NUMBER: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2881
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-944-1
Alignment Scores:
Pred. No.: 7.38e-54 Length: 2881
Score: 622.50 Matches: 109
Percent Similarity: 94.07% Conservative: 2
Best Local Similarity: 92.37% Mismatches: 6
Query Match: 91.28% Indels: 1
DB: 10 Gaps: 1

US-10-624-932c-2_COPY_232_348 (1-117) x US-09-970-944-1 (1-2881)
Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 780 AGCGCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGTGGTGGTGGACGTCGACCGAGTGG 839
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 840 TCCGTCTGCAAGCCAGCTGTGGCGCGGTGGCAGAAACGGAGCCGAGCTGCACCAAC 899
Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenVal---GlnLysThrAla 59
Db 900 CCGGCGCTCTCAACGGGGGGCGCTTCTGTGAGGGGCAGAAATGTCATGATGCCGACCGTC 959
Qy 60 CysAlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCys 79
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; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 3
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-3

Alignment Scores:
Pred. No.: 1,15e-43 Length: 2860
Score: 523.00 Matches: 84
Percent Similarity: 82.05% Conservative: 12
Best Local Similarity: 71.79% Mismatches: 21
Query Match: 76.69% Indels: 0
DB: 17 Gaps: 0

US-10-624-932c-2_COPY_232_348 (1-117) x US-10-087-684-3 (1-2860)
Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 764 AGCACCACTGCCACCGTCATCGTCTACGTGAATGCGCGTGGTCCAGTCGGGCAGAGTGG 823
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 824 TCACCCCTGCTCCCAACCGCTGTGGCCGAGGCTGGCAGAAAGCGCACCCGGACCTGCACCAAC 883
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 884 CCGCTCCTCACTCAACGAGGGGCGCTTCTGCAGGGCCAGGCATTCCAGAGACCGCTTGC 943
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 944 ACCACCATCTGCCAGTCGATGGGCGTGGACGAGTGGAGCAAGTGGTCAAGCTGCGCAGC 1003
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 1004 ACTGAGTGTGCCCACTGGCGTAGCGGAGTGCATGGCGCCCGCCCGCCCGCCCGAGGCG 1063
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1064 CGTGACTGCACGGGACGCTCTCGACTCTAAGAACTGCACAGATGGGCTG 1114

RESULT 9
US-10-218-779-1
; Sequence 1, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan

; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Baha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,-926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-218-779-1

Alignment Scores:
Pred. No.: 1,15e-43 Length: 2860
Score: 523.00 Matches: 84
Percent Similarity: 82.05% Conservative: 12
Best Local Similarity: 71.79% Mismatches: 21
Query Match: 76.69% Indels: 0
DB: 17 Gaps: 0

US-10-624-932c-2_COPY_232_348 (1-117) x US-10-218-779-1 (1-2860)
Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 764 AGCACCACTGCCACCGTCATCGTCTACGTGAATGCGCGTGGTCCAGTCGGGCAGAGTGG 823
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 824 TCACCCCTGCTCCCAACCGCTGTGGCCGAGGCTGGCAGAAAGCGCACCCGGACCTGCACCAAC 883
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 884 CCGCTCCTCACTCAACGAGGGGCGCTTCTGCAGGGCCAGGCATTCCAGAGACCGCTTGC 943
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 944 ACCACCATCTGCCAGTCGATGGGCGTGGACGAGTGGAGCAAGTGGTCAAGCTGCGCAGC 1003
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 1004 ACTGAGTGTGCCCACTGGCGTAGCGGAGTGCATGGCGCCCGCCCGCCCGAGGCG 1063
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1064 CGTGACTGCACGGGACGCTCTCGACTCTAAGAACTGCACAGATGGGCTG 1114

RESULT 10
US-10-218-779-3
; Sequence 3, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
```



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Qy 1 SerAlaSerAlaValIleValTyxValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 736 AGCACCACTGCCACCGTCATCGTCTAGTGATGATGGCGGTGGTCCAGCTGGCGAGAGTGG 795
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 796 TCACCCCTGCTCCAAACCGCTGTGGCCGAGGCTGGCGAGAAGCGCACCCGCGACCTGCACCAAC 855
Qy 41 ProAlaProLeuAnGlyGlyAlaPheCysGluGlyGlnAnValGlnLysThrAlaCys 60
Db 856 CCGCGCTCCACTCAACGAGGGGCGCTTCTGGAGGGCCAGGCATTCCAGAAAGACCGCGCTGC 915
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 916 ACCACCATCTGCCAGTCGATGGGCGCTGGACGAGTGGAGCAAGTGTGAGCCTGGCAGC 975
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 976 ACTGAGTGTGCCACTGGCGTAGCGCGAGTGCATGGCGCCGCCACCCAGAACCGGAGGC 1035
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAnCysThrSerAspLeu 117
Db 1036 CGTGACTGCAGCGGGACGCTGCTCGACTCTTAAGAACTGCACAGATGGGCTG 1086

RESULT 12
US-09-972-211-55
; Sequence 55, Application US/09972211
; Publication No. US20040048245A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zernhusen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Stone, David J
; APPLICANT: Smithson, Glennnda
; APPLICANT: Szekeres Jr, Edward S
; TITLE OF INVENTION: No. US20040048245A1el Human Proteins, Polynucleotides Encoding Th
; TITLE OF INVENTION: Methods Of Using The Same
; FILE REFERENCE: 21402-141
; CURRENT APPLICATION NUMBER: US/09/972,211
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,325
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,323
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,400
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,397
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,401
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,379
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,402
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 30/238,384
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,373
; PRIOR FILING DATE: 2000-10-06
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; PRIOR APPLICATION NUMBER: 60/238,372
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,383
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,382
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/275,892
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/296,860
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 2995
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(2901)
US-09-972-211-55
Alignment Scores:
Pred. No.: 1,21e-43
Score: 523.00
Percent Similarity: 82.05%
Best Local Similarity: 71.79%
Query Match: 76.69%
DB: 11
Length: 2995
Matches: 84
Conservative: 12
Mismatches: 21
Indels: 0
Gaps: 0
US-10-624-932c-2_COPY_232_348 (1-117) x US-09-972-211-55 (1-2995)
Qy 1 SerAlaSerAlaValIleValTyxValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 784 AGCACCACTGCCACCGTCATCGTCTAGTGATGATGGCGGTGGTCCAGCTGGCGAGAGTGG 843
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 844 TCACCCCTGCTCCAAACCGCTGTGGCCGAGGCTGGCGAGAAGCGCACCCGCGACCTGCACCAAC 903
Qy 41 ProAlaProLeuAnGlyGlyAlaPheCysGluGlyGlnAnValGlnLysThrAlaCys 60
Db 904 CCGCGCTCCACTCAACGAGGGGCGCTTCTGGAGGGCCAGGCATTCCAGAAAGACCGCGCTGC 963
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 964 ACCACCATCTGCCAGTCGATGGGCGTGGACGAGTGGAGCAAGTGTTCAGCCTGCAGC 1023
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 1024 ACTGAGTGTGCCACTGGCGTAGCGCGAGTGCATGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1083
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAnCysThrSerAspLeu 117
Db 1084 CGTGACTGCAGCGGGACGCTGCTCGACTCTTAAGAACTGCACAGATGGGCTG 1134

RESULT 13
US-10-096-625-55
; Sequence 55, Application US/10096625
; Publication No. US20040068095A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zernhusen, Bryan D
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Spytek, Kimberly Ann
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit
```


Db 829 CCCGCTCCACTCAACGGAGGGCGCTTCTGCGAGGGCCAGGCAATTCACAGAACCGCCTGC 888
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerProTrpSerLeuAsnGlyGly 80
Db 889 ACCACCATCTCCCGAGTCGATGGGCGGTGGAGCGAGTGGAGCAAGTGTCAAGCTGCAGC 948
Qy 81 LeuAspCysThrHisTrpArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 949 ACTGAGTGTGCCACTGCGTAGCGCGAGTGCATGGGCGCCGCCACCCAGAACGGAGGC 1008
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1009 CGTGACTGCAGCGGAGCGCTGCTCGACTCTAAGAACTGCACAGATGGGCTG 1059

RESULT 15

US-10-295-027-1123
; Sequence 1123, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1123
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-1123

Alignment Scores:

Pred. No.:	1.42e-43	Length:	3501
Score:	523.00	Matches:	84
Percent Similarity:	82.05%	Conservative:	12
Best Local Similarity:	71.79%	Mismatches:	21
Query Match:	76.69%	Indels:	0
DB:	17	Gaps:	0

US-10-624-932C-2_COPY_232_348 (1-117) x US-10-295-027-1123 (1-3501)

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Db 721 AGACCACTGCCACCGTCATCGTCTACGTGAATGGCGGCTGGTCCAGCTGGGCGAGTGG 780
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 781 TCACCTGTCTCCAAACCGCTGTGGCCGAGGCTGGCAGAAGCGCACCCCGGACCTGCACCAAC 840
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 841 CCCGCTCCACTCAACGGAGGGGCTTCTGCGAGGGCCAGGCATTCACAGAACCGCCTGC 900
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLeuAspGly 80
Db 901 ACCACCATCTGCCAGTTCGATGGGGCTGGACGGAGTGGAGCAAGTGGTCAAGCTGCAGC 960
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 961 ACTGAGTGTGCCACTGGCGTAGCCGCGAGTGCATGGCGGCCCCGCCACCCAGAACGGAGGC 1020
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 1021 CGTGACTGCAGCGGAGCGCTGCTCGACTCTAAGAACTGCACAGATGGGCTG 1071

Search completed: September 9, 2005, 18:52:13

Job time : 1175.56 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 22:38:37 ; Search time 3850.68 Seconds
(without alignments)
1156.553 Million cell updates/sec

Title: US-10-624-932c-2_COPY_232_348

Perfect score: 682
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=EST -Qfmt=fastap -SUffix=first -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=560 -MINLEN=0 -MAXLEN=2000000000
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-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gesi:
9: gb_gesi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	531	77.9	875	7	CO807001 AGENCOURT
5	531	77.9	2791	9	AY406493
6	531	77.9	3790	3	AK031655 Mus muscu
7	529	77.6	709	1	AJ729963 AJ729963
8	523	76.7	2532	9	AY411747 Homo sapi
9	522	76.5	693	6	CB246544 UI-M-FIO-

10	522	76.5	2532	9	AY411749	AY411749 Mus muscu
11	522	76.5	3866	3	AK018177	AK018177 Mus muscu
12	520	76.2	594	6	CA771550	CA771550 io72f10.Y
13	508	74.5	856	7	CN164143	CN164143 994266 MA
14	505	74.0	678	2	BF098738	BF098738 601750874
15	502	73.6	746	5	BX872585	BX872585 BX872585
16	502	73.6	751	5	BX871388	BX871388 BX871388
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22	485	71.1	681	2	BF313643	BF313643 601900292
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24	485	71.1	2775	9	AY401469	AY401469 Homo sapi
25	484	71.0	801	7	CV110922	CV110922 AGENCOURT
26	484	71.0	2775	9	AY401471	AY401471 Mus muscu
27	466	68.3	774	5	BH365958	BH365958 603785840
28	439	64.4	679	7	CO045001	CO045001 UI-M-GIO-
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31	429	62.9	2532	9	AY411748	AY411748 Pan trogl
32	399	58.5	969	2	BF206813	BF206813 601870209
33	388	56.9	605	5	EX913103	EX913103 EX913103
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37	357	52.3	676	5	BM353356	BM353356 BM353356
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45	327.5	48.0	1532	3	BC033727	BC033727 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS BX452510 Homo sapiens ADULT BRAIN Homo sapiens CDNA clone
DEFINITION CS0DN001YE16 5-PRIME, mRNA sequence.
ACCESSION BX452510
VERSION BX452510.2 GI:47063451
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 548)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 22, 2003 this sequence version replaced gi:31026396.
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five cloned
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3529.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS0BAG0692F06_CS06574_1&c=3529.f

FEATURES
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/mol_type="mrna"
 /db_xref="taxon:9606"
 /clone="CSODN001YE16"
 /tissue_type="ADULT BRAIN"
 /dev_stage="adult"
 /clone_lib="Homo sapiens ADULT BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; let strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 4.48e-39 Length: 548
 Score: 594.00 Matches: 102
 Percent Similarity: 92.11% Conservative: 3
 Best Local Similarity: 89.47% Mismatches: 9
 Query Match: 87.10% Indels: 0
 DB: 5 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x BX452510 (1-548)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTyrSerThrTyrThrGluTyr 20
 Db 188 AGCGCCTCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGTCGACGCGGAGTGG 247
 Qy 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAsn 40
 Db 248 TCCGTCTCAGCGCCAGCTGTGGCGCGGTGGCAGAAACGAGCGCGAGCTGCACCAAC 307
 Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGlyGlnAenValGlnLysThrAlaCys 60
 Db 308 CGCGCGCTGTCAACGGGGCGCTTCTGTGAGGGGCGAGATGTTCAAGAAACAGCCCTGC 367
 Qy 61 AlaThrLeuCysProValAspGlySerTyrProTyrSerTyrSerTyrSerAlaCysGly 80
 Db 368 GCCACCTGTGCCCGATGACGGTAGATGGAGCGCGTGGAGCAAGTGGTCTGTGGG 427
 Qy 81 LeuAspCysThrHisTyrArgSerArgGlyCysSerAspProAlaProArgAsnGlyGly 100
 Db 428 CTGGACTGCACCCACTGGCGGAGCGTGTGAGTGTCTGACCCAGTACCCCGCAACGGAGGG 487
 Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThr 114
 Db 488 GTGAGTGTCAAGTTTCTGCTCTGTTACCCCTGTTCTGTTCC 529

RESULT 2

LOCUS AY406491 2802 bp DNA linear GSS 15-DEC-2003
 DEFINITION Homo sapiens UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
 ACCESSION AY406491
 VERSION AY406491.1 GI:39762465
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2802)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED

14671302

REFERENCE

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE

JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering them based on alignment.

COMMENT

FEATURES
 source
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 <1..>2802
 /gene="UNC5C"
 /locus_tag="HCM2575"

ORIGIN

Alignment Scores:
 Pred. No.: 1.23e-33 Length: 2802
 Score: 539.00 Matches: 86
 Percent Similarity: 86.32% Conservative: 15
 Best Local Similarity: 73.50% Mismatches: 16
 Query Match: 79.03% Indels: 0
 DB: 9 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x AY406491 (1-2802)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTyrSerThrTyrThrGluTyr 20
 Db 754 AGTCAACACTGCACCTGTCTATGTCAACGGTGGTGTCCACTGACCGAGTGG 813
 Qy 21 SerValCysSerAlaSerCysGlyArgGlyTyrGlnLysArgSerArgSerCysThrAsn 40
 Db 814 TCTGTGTAAACCCCGCTGTGGACGAGGTATCAGAAACGTACAGGACTTGTACCAAC 873
 Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGlyGlnAenValGlnLysThrAlaCys 60
 Db 874 CCGGACCACTCAATGGGGTGCCTTCTGTGAGGGCAGAGTGTGCAAAATAGCCTGT 933
 Qy 61 AlaThrLeuCysProValAspGlySerTyrProTyrSerTyrSerTyrSerAlaCysGly 80
 Db 934 ACTACGTATGCCAGTGGATGGAGTGGACGCCATGGAGCAAGTGGTCTACTTGTGGA 993
 Qy 81 LeuAspCysThrHisTyrArgSerArgGlyCysSerAspProAlaProArgAsnGlyGly 100
 Db 994 ACTGAGTGACCCACTGGCGCAGGAGGAGTGTGACGGCGCCAGCCCAAGATGGAGGC 1053
 Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
 Db 1054 AAGGACTGCGACGCGCTCTTGCATCCAGAACTGCACCTGATGGGCTT 1104

RESULT 3

LOCUS AY406492 2802 bp DNA linear GSS 15-DEC-2003
 DEFINITION Pan troglodytes UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
 ACCESSION AY406492
 VERSION AY406492.1 GI:39762466
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1 (bases 1 to 2802)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED

14671302

REFERENCE

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,


```

AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
TITLE        Inferring nonneutral evolution from human-chimp-mouse orthologous
              gene trios
JOURNAL      Science 302 (5652), 1960-1963 (2003)
PUBMED       14671302
REFERENCE    2 (bases 1 to 2791)
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
              Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
              Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
              Adams,M.D. and Cargill,M.
TITLE        Direct Submission
JOURNAL      Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
              Rockville, MD 20850, USA
COMMENT      This sequence was made by sequencing genomic exons and ordering
              them based on alignment.
FEATURES     Location/Qualifiers
              source          1..2791
                              /organism="Mus musculus"
                              /mol_type="genomic DNA"
                              /db_xref="taxon:10090"
              gene            <1..>2791
                              /gene="UNC5C"
                              /locus_tag="HCN2575"
ORIGIN
Alignment Scores:
Pred. No.:      5.56e-33      Length:      2791
Score:          531.00      Matches:    85
Percent Similarity: 85.47%      Conservative: 15
Best local Similarity: 72.65%      Mismatches: 17
Query Match:    77.86%      Indels:      0
DB:             9          Gaps:        0

US-10-624-932C-2_COPY_232_348 (1-117) x AY406493 (1-2791)

Qy  1 SerAlaSerAlaAlaValIleValTy-rValAnGlyGlyTrpSerThrTrpThrGluTrp 20
    ||| :|||
Db  743 AGCACCCAGCACCTGTCATCGTGTATGTTAATGTGGTGGTCCATCGTGCACAGATGG 802

Qy  21 SerValCysSerHisTrpArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
    ||| :|||
Db  803 TCTGTGTACACCCGCTGTGGCGGAGATATCAGAAACCCACAGACCTGCACCCAC 862

Qy  41 ProAlaProLeuAnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
    ||| :|||
Db  863 CCAGCCCCACTCAATGGTGGGCCCTTCTGTGAGGGGCAGAGTGTGCAGAAATAGCATGC 922

Qy  61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
    ||| :|||
Db  923 ACTACGTTATGTCAGTGGATGGTGGTGGGACTTCATGGAGCAAAATGGTCAACCTGTGGG 982

Qy  81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
    ||| :|||
Db  983 ACTGAATGACCCACTGGCGGACGAGGGAGGTGTACAGCACCCAGCCCCCAAGACGGGGGT 1042

Qy  101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
    ||| :|||
Db  1043 AAGGACTGTGATGGCTGGTCTCCATCCAAAGAACTGCACATGATGGGCTG 1093

RESULT 6
AK031655
LOCUS      AK031655      3790 bp      mRNA      linear      HTC 03-APR-2004
DEFINITION Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
              enriched library, clone:6030473H24 product:unc5 homolog (C.
              elegans) 3, full insert sequence.
ACCESSION AK031655
VERSION   AK031655.1 GI:26327502
KEYWORDS  HTC; CAP trapper.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE    Carninci,P. and Hayashizaki,Y.
              High-efficiency full-length cDNA cloning
              Meth. Enzymol. 303, 19-44 (1999)
              99279253
              10349636
2
REFERENCE    Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
              Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
              Normalization and subtraction of cap-trapper-selected cDNAs to
              prepare full-length cDNA libraries for rapid discovery of new genes
              Genome Res. 10 (10), 1617-1630 (2000)
              20499374
              11042159
3
REFERENCE    Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
              Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M.,
              Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
              Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
              Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
              Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
              Okazaki,Y., Muramatsu,M., Inoue,Y., Kiza,A. and Hayashizaki,Y.
              RIKEN integrated sequence analysis (RISA) system--384-format
              sequencing pipeline with 384 multicapillary sequencer
              Genome Res. 10 (11), 1757-1771 (2000)
              20530913
              11076861
4
REFERENCE    The RIKEN Genome Exploration Research Group Phase II Team and the
              FANTOM Consortium
              Functional annotation of a full-length mouse cDNA collection
              Nature 409, 685-690 (2001)
5
REFERENCE    The FANTOM Consortium and the RIKEN Genome Exploration Research
              Group Phase I & II Team.
              Analysis of the mouse transcriptome based on functional annotation
              of 60,770 full-length cDNAs
              Nature 420, 563-573 (2002)
6 (bases 1 to 3790)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,P., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,K., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp.
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
1..3790
/organism="Mus musculus"
/mol_type="mRNA"
FEATURES     source

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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 2532) Clark,A.G., Gланowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrieria,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 2532)
AUTHORS	Clark,A.G., Gланowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrieria,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
source	1..2532 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" !1..>2532 /locus tag="HCKM4327"
gene	

Alignment Scores:					
Pred. No.:	2.23e-32	Length:	2532		
Score:	523.00	Matches:	84		
Percent Similarity:	82.05%	Conservative:	12		
Best Local Similarity:	71.79%	Mismatches:	21		
Query Match:	76.69%	Indels:	0		
DB:	9	Gaps:	0		
US-10-624-932C-2_COPY_232_348 (1-117) x AY411747 (1-2532)					
Qy	1	SerAlaSerAlaAlaValIleValtyrValAenGlyGlyTrpSerThrTrrThrGluTrp	20		
Dd	400	AGCACCTGCACCGTCATGTCTACTGAATGGCGCTGGTCCAGCTGGCAGATGG	459		
Qy	21	SerValCySserAlaserCySclyArgGlyTrpGlnLyAsArgSerArgSerCysThrAen	40		
Dd	460	TCACCCTGCTCCAACCGCTGTGGCCAGGCTGGCAGAAGCGCACCCGGACCTGCACCAAC	519		
Qy	41	ProLalaProLeuaAnGLyGlyAlapheCySGluGlyGlnAenValcLnlystrHlacyS	60		
Dd	520	CCCCTCCACCTCAACGGAGGGGCCCTTCTCGAGGGCCAGGCCATTCCAGAAGACCCGCTGC	579		
Qy	61	AlaThrLeuCysProValAspDylSerTrpSerProTrpSerLystrTrpSerAlaCySgLy	80		
Dd	580	ACCACCATCTGCCAGTCGATGGGGCGTGACGGAGTGGAGCAAGTGGTCACGCTCGACG	639		
Qy	81	LeuAspCysThrHisTrpArpSerArgGluCySserAspProAlaProArgAenGlyGly	100		
Dd	640	ACTGAGTGTGCCCATCTGGCTAGCCGCGAGTCATGGCGCCCCCACCACCCAGAACCGAGGC	699		
Qy	101	GluGluCySgInGlyThrAspLeuAspThrArgAenCysThrSerAspLeu	117		
Dd	700	CGTGACTGACGGGACGCTGCTCGACTCTAAGAACTGCACAGATGGGCTG	750		
RESULT 9 CB246544 693 bp mRNA linear EST 09-JUL-2000					
LOCUS CB246544					
DEFINITION UI-M-P10-cdw-h-16-o-UI.r1 NIH_BMAP_P10 Mus musculus cDNA clone					
IMAGE:6835361 5', mRNA sequence.					
ACCESSION CB246544					
VERSION CB246544.1 GI:28368188					
KEYWORDS Est.					
SOURCE Mus musculus (house mouse)					

```

ORGANISM      Mus musculus
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE         NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL       National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT       Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-x@mail.nih.gov
              Tissue Procurement: Dr. Jim Lin, University of Iowa
              cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
              cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
              DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
              Clone Distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              This clone was contributed by the Brain Molecular Anatomy Project
              (BMAP)

FEATURES      Seq primer: pyX-5.
              Location/Qualifiers
                1..693
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                  /mol_type="mRNA"
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                  /db_xref="taxon:10090"
                  /clone="IMAGE:6835361"
                  /tissue_type="whole brain"
                  /lab_host="embryo 12.5dpc"
                  /dev_stage="DH10B (T1 phage resistant)"
                  /clone_lib="NIH BMAP F10"
                  /note="Organ: Brain; Vector: pYX- Asc; Site 1: Ecor I;
                  Site 2: Not I; The library was constructed according
                  Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                  1996. Denatured RNA was size fractionated on a 1% agarose
                  gel. First strand cDNA synthesis was primed with oligo-dT
                  primer containing a Not I site. Double strand cDNA was
                  size selected according to mRNA size fraction, ligated
                  with Ecor I adaptor, digested with NotI and then cloned
                  directionally into pYX-Asc vector. The library tag
                  sequence located between the Not I site and the polyA tail
                  is CAGCACGAC. This library was created for the University
                  Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                  Developing Mouse Nervous System', supported by National
                  Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                  program coordinator."

```

```

program Coordinator;

ORIGIN

Alignment Scores:
Pred. No.:      4.99e-33          Length:        693
Score:         522.00           Matches:       84
Percent Similarity: 82.05%       Conservative:   12
Best Local Similarity: 71.79%    Mismatches:   21
Query Match:    76.54%          Indels:        0
DB:             6              Gaps:          0


US-10-624-932C-2_COPY_232_348 (1-117) x CB246544 (1-693)

Qy      1 SerAlaSerAlaAlavalleValrYrvAlasnglyGlyTrpSerThrTpThrGlufrrp 20
      ||| :|| 
Db     172 AGCACCGGCACAGTCATCGTCTATGTGAATGGAGGCTGGTCCAGCTGGGCACAGATTGG 231

Qy     21 ServAlCysserAlaserCysGlyVArgGlyTrpGlnIlysAArgSerArgSerCystrhaen 40
      ||| :|| 
Db     232 TCACCCTGTTTCCAATCGCTGGGCCGAGCGTGGCAGAAGCGTA CTGGACCTGCACCAAT 291

Qy     41 ProAlaProLeuAsnGlyGVlAlapheCysGluGlyGlnAsnValGlnIlynsthrAlaCys 60
      ||| :|| 
Db     292 CCAGCCCCACTCAATGNGGGCGCCCTCTGTGARGGACAGGCCCTTC CAGNAGACAGCTTGC 351

Qy     61 AlaThrLeuCysProValAspGlyserTrpSerProflrpSerLyfTrpSerAlaCysGly 80
      ||| :|| 
Db    352 ACCACCTGTGTCACAGTGATGGAGCGTGACCCAGTCGACCAAGTGGCTCGCTGCAGC 411

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Qy 81 LeuaspCysThrHisTrpArgSerArgGluCySerAspProAlaProArgAsnGlycyl 100
:::|||||
Db 640 ACAGAGTGTGGCGACTGCACGCCGAGTGCTGTCATGGCCACGCCACCCAGAACGGAGCC 699

Qy 101 GluGlucCySeGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
:::|||||
Db 700 CGTGACTGCACGGGACGCTACTTTGACTCCAAGAACAATGCACCTGATGGCGTG 750

RESULT 11

AKO18177 3866 bp mRNA linear HTC 03-APR-2004

LOCUS Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:630415E02 product:TRANSMEMBRANE RECEPTOR UNC5H2 homolog [Rattus norvegicus], full insert sequence.

ACCESSION AKO18177.1 GI:12857775

VERSION HTK; CAP trapper.

KEYWORDS Mus musculus

SOURCE Mus musculus

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
99279253

REFERENCE 2 10349636

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL 20493974

MEDLINE 11042159

REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Onoda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J., Yokozaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL 20530913

MEDLINE 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
6 (bases 1 to 3866)

ADACHI, J., AIZAWA, K., AKAHARA, S., AKIMURA, T., ARAI, A., AONO, H., ARAKAWA, T., BONO, H., CARNINCI, P., FUKUDA, S., FUKUNISHI, Y., FUNO, M., HANGAKI, T., HARA, A., HAYATSU, N., HIRAMOTO, K., HIRAOKA, T., HORI, F., IMOTANI, K., ISHII, Y., ITOH, M., IZAWA, M., KASUKAWA, T., KATO, H., KAWAI, J., KOJIMA, Y., KONNO, H., KODA, M., KOYA, S., KURIHARA, C., MATSUMOTO, T., MIYAZAKI, A., NISHI, K., NOMURA, K., NUMAZAKI, R., OHNO, M., OKAZAKI, Y., OKIDO, T., OWA, C., SAITO, H., SAITO, R., SAKAI, C., SAKAI, K., SANO, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tegawa, A., Takahashi, F., Tanaka, T., Yoshino, Y., Toyota, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permut Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@ingate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

Alignment Scores:
Pred. No.: 5,96e-33 Length: 594
Score: 520.00 Matches: 83
Percent Similarity: 82.0% Conservative: 13
Best Local Similarity: 70.94% Mismatches: 21
Query Match: 76.25% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x CA771550 (1-594)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAenGlyGlyTrpSerThrTrpThrGluTrp 20
Db 187 AGCACCCTGCGCCACCGTCATGCTACTTGAATGGCGCTGCTCCAGCTGGCGAGAGTGG 246
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 247 TCACCTCTGCTCAACCGCTGTGGCGAGCGCTGGCAGAACGCGACCCGACCTGCACCAAC 306
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 307 CCGCTCCACTCAACGAGGGGCTTCTGCGAGGGCCAGGCAATCCAGAACCGCCCTGC 366
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 367 ACCACCTCTGCCAGTGCATGGGCGGTGGAGCGAGTGGCAAGTGTCCAGCTGCAGC 426
Qy 81 LeuAspCysThrHisTrpArgSerHrgLysCysSerAspProAlaProArgAsnGlyGly 100
Db 427 ACTGAGTGTGCCACTGCGTAGCGCGAGTGCATGGCGGCCCCCAACCCAGAACCGAGGC 486
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArgAsnCysThrSerAspLeu 117
Db 487 CGTGACTGACGGGAGCGCTGCTCACTCTTAGAACTGCACAGATGGGCTG 537

RESULT 13

LOCUS CN164143 856 bp mRNA linear EST 02-APR-2004
DEFINITION 994266 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION CN164143
VERSION CN164143.1 GI:46178573

KEYWORDS

EST.

SOURCE

Sus scrofa (pig)

ORGANISM

Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (Bases 1 to 856)

Smith.T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,

Nonneman,D.J., Wray,J.E. and Keele,J.W.

Porcine EST collection using a normalized library constructed from

embryos representing early developmental stages

Unpublished (2003)

CONTACT: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and

trimmed with the aid of the trim_alt option. Vector identified with

cross match v0.990329.

Plate: TMW8062 row: N column: 14

Seq primer: GTAATACGACTCATTATAGG.

Location/Qualifiers

1..856

FEATURES

source

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4PIG"
/note="vector: pCDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

ORIGIN

Alignment Scores:
Pred. No.: 9,28e-32 Length: 856
Score: 508.00 Matches: 81
Percent Similarity: 86.4% Conservative: 15
Best Local Similarity: 72.97% Mismatches: 15
Query Match: 74.4% Indels: 0
DB: 7 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x CN164143 (1-856)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAenGlyGlyTrpSerThrTrpThrGluTrp 20
Db 524 AGCACCCTGCGCCACCGTCATGCTACTTGAATGGCGCTGCTCCAGCTGGCGAGTGG 583
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 584 TCTGTGTGTAATAGCGCTGTGGAGCGGTATCAGAAGCGCACAAAGACCTGCACCAAT 643
Qy 41 ProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsnValGlnLysThrAlaCys 60
Db 644 CCAGCCCCACTCAATGGTGGTCCCTTCTGTAAGGGCAGAGTGTGCAGAAATATGCTGT 703
Qy 61 AlaThrLeuCysProValAspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 704 ACCAGTGTGCCAGTGGATGGCAGATGGACCTCATGAGTGAAGTGTGACCTGCGGG 763
Qy 81 LeuAspCysThrHisTrpArgSerArgGluCysSerAspProAlaProArgAsnGlyGly 100
Db 764 ACCAGTGCACACACTGGCGCAGAGGAGTGCACAGCACCAGCCCCCAAGAATGGAGGC 823
Qy 101 GluGluCysGlnGlyThrAspLeuAspThrArg 111
Db 824 AAGGACTGCGATGGCTGCTTACAGTCCAAG 856

RESULT 14

LOCUS BF098738

DEFINITION BF098738 678 bp mRNA linear EST 19-OCT-2000

ACCESSION BF098738

VERSION BF098738.1 GI:10881264

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Bases 1 to 678)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM9171 row: c column: 19

High quality sequence stop: 634.

Location/Qualifiers

FEATURES

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source
1. .678
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/mol_type="mRNA"
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/db_xref="IMAGE:3978570"
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/dev_stage="3 months, virgin"
/lab_host="DH10B"
/clone_lib="NCI CGAP Maml"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sali; Site 2: Not1; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN
Alignment Scores:
Pred. No.: 1.21e-31 Length: 678
Score: 505.00 Matches: 80
Percent Similarity: 82.73% Conservative: 11
Best Local Similarity: 72.73% Mismatches: 19
Query Match: 74.05% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x BF098738 (1-678)

Qy 8 ValtYrVallAenGlyGlyTrpSerThrTrpThrGluTrpSerValCysSerAlaSerCys 27
Db 2 GTCTATGTGAATGAGGCGTGTCCAGCTGGCGAGAGTGGTCCACCCTGTTCCTCAATCGCTGT 61
Qy 28 GlyArgGlyTrpGlnLysAenArgSerCysThrAenProAlaProLeuAenGlyGly 47
Db 62 GGCCGAGCTGGCAGAGCGTACTCGGACCTGACCAATCCAGCCCTCAATGAGGC 121
Qy 48 AlaPheCysGluGlyGlnAenValGlnLysThrAlaCysAlaThrLeuCysProValAasp 67
Db 122 GCCTTCTGTGAGGACAGAGCGCTTCAGAGACAGACGCTTGACACCGTGTGCCAGTGGAT 181
Qy 68 GlySerTrpSerProTrpSerLysTrpSerLysCysGlyLeuAenCysThrHisTrpArg 87
Db 182 GGACGCTGGACCGAGTGGAGCAAGTGTCTCCCTGCACGACACAGAGTGGCGCATGGCGC 241
Qy 88 SerArgGluCysSerAaspProAlaProArgAenGlyGlyGluCysGlnGlyThrAasp 107
Db 242 AGCCGCGAGTGCATGCGACCGCCACCCAGACGAGGCGCGTGACTGCAGCGGACGCTA 301
Qy 108 LeuAaspThrArgAenCysThrSerAaspLeu 117
Db 302 CTTGACTCCAAGAACTGCCTGATGGGCTG 331

RESULT 15
BX872585 746 bp mRNA linear EST 24-MAY-2004
LOCUS BX872585 tcbk Oncorhynchus mykiss cdna clone tcbk0009c.j.16 5prim, mRNA sequence.
ACCESSION BX872585
VERSION BX872585.2 GI:42787249
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 746)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cdna libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
JOURNAL On Dec 17, 2003 this sequence version replaced gi:39999678.
COMMENT Contact: Guiguen Y
INRA - SCRIBE
Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
```

```
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0009 row: j column: 16
Seq primer: M13R.
Location/Qualifiers
source
1. .746
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/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="tcbk"
/notes="Vector: pT73D-pac; AGENAE Rainbow trout
multi-tissues - normalized + 2 subtractions; Clone
distribution : AGENAE Resource centre. Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN
Alignment Scores:
Pred. No.: 2.41e-31 Length: 746
Score: 502.00 Matches: 81
Percent Similarity: 82.91% Conservative: 16
Best Local Similarity: 69.23% Mismatches: 20
Query Match: 73.61% Indels: 0
DB: 5 Gaps: 0

US-10-624-932C-2_COPY_232_348 (1-117) x BX872585 (1-746)

Qy 1 SerAlaSerAlaAlaValIleValTyrValAsnGlyGlyTrpSerThrTrpThrGluTrp 20
Db 331 AGTACCACCTGCTACTGTATTGTCTATGTGAACGGCGCTGTTCGACATGCACAGAGTGG 390
Qy 21 SerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArgSerArgSerCysThrAsn 40
Db 391 TCAGTGTGTAAACAGTCGCTGTGGCGCGGTGTACCAAAAGCGGTACCCGACGCTGTACCAAT 450
Qy 41 ProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAenValGlnLysThrAlaCys 60
Db 451 CCGCCCGCTCAACGAGGAGGAGCCCTGTGTGATGACAGGACAGGAGTGGAGTGGTCTACTTGGT 510
Qy 61 AlaThrLeuCysProValAaspGlySerTrpSerProTrpSerLysTrpSerAlaCysGly 80
Db 511 ACCTCCCTCTGCACCTGTTGACGGGTTGTGGACAGAGTGGAGTAAAGTGTCTACTTGGT 570
Qy 81 LeuAaspCysThrHisTrpArgSerArgGluCysSerAaspProAlaProArgAenGlyGly 100
Db 571 ACAGAGTGCACTCACTGGCGCAGAGAGAAATGCAATGCCCTGCACCAAAATGAGGC 630
Qy 101 GluGluCysGlnGlyThrAaspLeuAaspThrArgAenCysThrSerAaspLeu 117
Db 631 AAGGACTGCGAGGGGTATGGTCTACAGTCCAGAACTGTACTGACGGACTC 681

Search completed: September 9, 2005, 04:40:39
Job time : 3857.68 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:47:02 ; Search time 2077.73 Seconds
(without alignments)
1166.064 Million cell updates/sec

Title: US-10-624-932C-2_COPY_246_295

Perfect score: 290

Sequence: 1 STWTSEVSCSACRGWQKR.....NGGAFCEQNVQTKATATLC 50

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n model -DEV=xlh
-Q/cgn2_1/USPTO.spool_h/US10624932/runat_08092005_161705_15773/app_query.fasta_1.1386
-DB=GenEmbl -QWMT=fastcap -SUPFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=spt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CGN 1.1 7509 @runat_08092005_161705_15773 -NCPU=6 -ICPU=3
-NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
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3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sw.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290	100.0	2697	6	AX268596 Sequence
2	290	100.0	2697	6	AX451852 Sequence
3	290	100.0	2697	10	U87305 Rattus norv
4	290	100.0	2752	6	AX449572 Sequence

5	290	100.0	2784	6	CQ730306	Sequence
6	290	100.0	3014	6	BD057524	Netrin re
7	290	100.0	3992	10	MMU487852	AJ487852 Mus muscu
8	290	100.0	4294	10	AK122575	Mus muscu
9	290	100.0	121282	9	AC027318	AC027318 Homo sapi
10	290	100.0	166534	2	AC034209	AC034209 Homo sapi
11	290	100.0	168168	2	AC012283	AC012283 Homo sapi
12	290	100.0	231407	2	AC139592	AC139592 Rattus no
13	290	100.0	242128	2	AC123700	AC123700 Mus muscu
14	249	85.9	2270	9	BC041156	BC041156 Homo sapi
15	249	85.9	2612	6	CQ881064	Sequence
16	249	85.9	2780	6	CQ881054	Sequence
17	249	85.9	2962	5	AY187310	Gallus ga
18	249	85.9	2986	6	CQ881052	Sequence
19	249	85.9	3646	6	CQ881060	Sequence
20	249	85.9	3646	9	AF055634	Homo sapi
21	249	85.9	9299	10	MMU72634	U72634 Mus musculu
22	249	85.9	159206	9	AC098584	Homo sapi
23	249	85.9	168940	2	AC102307	Mus muscu
24	249	85.9	191935	2	AC114747	AC114747 Homo sapi
25	244	84.1	9328	10	AB118026	AB118026 Rattus no
26	244	84.1	250375	2	AC131167	AC131167 Rattus no
27	243	83.8	2881	6	AX527916	Sequence
28	239	82.4	168	6	AX800695	Sequence
29	239	82.4	2585	6	CQ842137	Sequence
30	239	82.4	2585	9	AK122615	Homo sapi
31	239	82.4	2625	6	CQ721377	Sequence
32	239	82.4	2661	6	AX800717	Sequence
33	239	82.4	2860	6	AX686445	Sequence
34	239	82.4	2860	6	AX686447	Sequence
35	239	82.4	2868	6	AX800719	Sequence
36	239	82.4	2895	6	AX512281	Sequence
37	239	82.4	2995	6	AX497288	Sequence
38	239	82.4	3252	9	AY358147	Homo sapi
39	239	82.4	3770	9	AY126437	Homo sapi
40	239	82.4	3884	6	AX528525	Sequence
41	239	82.4	3884	6	AX464012	Sequence
42	239	82.4	3884	9	AY358351	Homo sapi
43	239	82.4	3933	6	CQ850929	Sequence
44	239	82.4	3933	9	AK128132	Homo sapi
45	239	82.4	3935	9	AB096256	Homo sapi

ALIGNMENTS

RESULT 1	AX268596	Sequence 15 from Patent WO01/5440.	2697 bp	DNA	linear	PAT 29-OCT-2001
LOCUS	AX268596	Sequence 15 from Patent WO01/5440.				
DEFINITION	AX268596					
ACCESSION	AX268596					
VERSION	AX268596.1	GI:16541710				
KEYWORDS						
SOURCE	Rattus sp.					
ORGANISM	Rattus sp.					
REFERENCE	1					
AUTHORS	Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and Pratt,J.Y.					
TITLE	Schizophrenia related genes					
JOURNAL	Patent: WO 01/5440-A 15 11-OCT-2001;					
FEATURES	WELFIDE CORPORATION (JP)					
source	Location/Qualifiers					
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ORIGIN						
Alignment Scores:						
Pred. No.:	1.89e-19	Length:	2697			
Score:	290.00	Matches:	50			


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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AX268596 (1-2697)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGAGTGGTCCGCTGTCAGAGCCAGCTGTGGCGCTGGTGGCAGAAACGG 795

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCCGGAGCTGCACCAACCCGCGACCTCTCAACGGGGCGCTTCTGTGAGGGGCAGAA 855

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAACAGAGCTGCGCCACTCTGTGC 885

RESULT 2
AX451652
LOCUS AX451652 2697 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1 from Patent WO0233080.
ACCESSION AX451652
VERSION AX451652.1 GI:21698587
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Koehler, R.H.
TITLE Regulation of human netrin binding membrane receptor unc5h-1
JOURNAL Patent: WO 0233080-A 1 25-APR-2002;
Bayer Aktiengesellschaft (DE)
FEATURES
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1..2697
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/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1..88e-19 Length: 2697
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AX451652 (1-2697)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
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Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCCGGAGCTGCACCAACCCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGCAGAA 855

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAACAGAGCTGCGCCACTCTGTGC 885

RESULT 3
RNU87305
LOCUS RNU87305 2697 bp mRNA linear ROD 15-MAY-1997
DEFINITION Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds.
ACCESSION U87305
VERSION U87305.1 GI:2055391
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 2697)
Leonardo, E.D., Hinch, L., Masu, M., Keino-Masu, K., Ackerman, S.L. and
Tessier-Lavigne, M.
Vertebrate homologues of C. elegans UNC-5 are candidate netrin
receptors
Nature 386 (6627), 833-838 (1997)
97271897
9126742
2 (bases 1 to 2697)
Leonardo, E.D., Hinch, L., Masu, M., Keino-Masu, K. and
Tessier-Lavigne, M.
Direct Submission
Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus, San
Francisco, CA 94143-0452, USA
Location/Qualifiers
1..2697
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SLQCGVILPCRPPEGIPPAEWEMLRNEDLVPSLDPNVYITRHSLVVROARLADTAN
YTCVAKNIVARRESTAAVIVYNGWSWTSVSCASCGRWKKSRCTNPAPLN
GGAFCEQNVQKTACATLCEVDGWSKWSACGLDCTHWRSECDPAPRNGECC
RGADLDTRNCTDCLHATSPEDVALYIGLVAVAVCLFLLALLGLIYCRKEGLDS
DVADSSLTGTFQSVISKADNPHELLTQDPLSTTTTQGSLSRQDQPGPKFOL
SNGLHSLPLSGSRHTLHSSPTSEADFVSRSTONYFRSLPRTSNMAYGTNFNLAG
RLMIPNTGISLLIPPDPAIPRGKIYEIYLTHKPEDVRLPLAGCQTLLSPVSCGPGV
LLTRPVILAMDHCPEPSDPSLRKKQSCGSEWEDVHLIGSESPSHLYTCQLEAGAC
YVFTEQGLRFALVGEALVSAATKRLRLLLFPVACTSLSEYNIRVYLHDTHDALKEV
QLEKQLCGQLIQEPRVLHFRLSYHNLRLSHDVPSSLWKSLLVSYQEIYFFHIWNGT
QOYLHCTFTLERINASTDLACKVWQVEGDGQSFNINFTKDTFAELLALLESQ
GVPALVGPSAKIPFLIRQKIASLDPPCSRGDWRTLAOKLHLDLSLSPFASKPSPT
AMINLWEARHPFNGNLQQLAAVAGLQDQDAGLFTVSEAC"

ORIGIN
Alignment Scores:
Pred. No.: 1..88e-19 Length: 2697
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x RNU87305 (1-2697)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGAGTGGTCCGCTGTCAGAGCCAGCTGTGGCGCTGGCAGAAACGG 795

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCCGGAGCTGCACCAACCCGCGACCTCTCAACGGGGCGCTTCTGTGAGGGGCAGAA 855

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAACAGAGCTGCGCCACTCTGTGC 885

RESULT 4
AX449572
LOCUS AX449572 2752 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1 from Patent WO0210216.

```



```
ACCESSION AX449572
VERSION AX449572.1 GI:21698195
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Padigaru, M., Mezes, P., Mishra, V., Burgess, C., Casman, S.,
Grosse, W.M., Alsbrook, J.P., Lepley, D.M., Gerlach, V.L.,
MacDougall, J.R. and Smithson, G.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0210216-A 1 07-FEB-2002;
FEATURES Curagen Corporation (US)
source Location/Qualifiers
1..2752
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1.91e-19 Length: 2752
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AX449572 (1-2752)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 781 TCGACGTGGACCGAGTGGTCCGCTCTGCAGCGCCAGCTGTGGCGGGCTGGCAGAAACGG 840
Qy 21 SerArgSerCysThrAsnProAlaProLeuAenGlyAlaPheCysGluGlyGlnAen 40
Db 841 AGCCGGAGCTGCACCAACCGCGCCTCTCAACGGGGGGCGCTTCTGTGAGGGGGCAGAAT 900
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 901 GTCCAGAAACAGCCTGCCACCCTGTGTC 930

RESULT 5
LOCUS CQ730306 2784 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 16240 from Patent WO02068579.
ACCESSION CQ730306
VERSION CQ730306.1 GI:42303801
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 16240 06-SEP-2002;
FEATURES PE Corporation (NY) (US)
source Location/Qualifiers
1..2784
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1.94e-19 Length: 2784
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

ACCESSION AX449572
VERSION AX449572.1 GI:21698195
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Padigaru, M., Mezes, P., Mishra, V., Burgess, C., Casman, S.,
Grosse, W.M., Alsbrook, J.P., Lepley, D.M., Gerlach, V.L.,
MacDougall, J.R. and Smithson, G.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0210216-A 1 07-FEB-2002;
FEATURES Curagen Corporation (US)
source Location/Qualifiers
1..2752
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1.91e-19 Length: 2752
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x CQ730306 (1-2784)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 823 TCGACGTGGACCGAGTGGTCCGCTCTGCAGCGCCAGCTGTGGCGGGCTGGCAGAAACGG 882
Qy 21 SerArgSerCysThrAsnProAlaProLeuAenGlyAlaPheCysGluGlyGlnAen 40
Db 883 AGCCGGAGCTGCACCAACCGCGCCTCTCAACGGGGGGCGCTTCTGTGAGGGGGCAGAAT 942
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 943 GTCCAGAAACAGCCTGCCACCCTGTGTC 972

RESULT 6
LOCUS BD057524 3014 bp DNA linear PAT 27-AUG-2002
DEFINITION Netrin receptors.
ACCESSION BD057524
VERSION BD057524.1 GI:22603130
KEYWORDS JP 2001505062-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 3014)
AUTHORS Lavigne, M.T., Leonardo, D.E., Hinck, L., Masu, M. and Masu, K.K.
TITLE Netrin receptors
JOURNAL Patent: JP 2001505062-A 1 17-APR-2001;
COMMENT THE REGENTS OF THE UNIV OF CALIFORNIA
PN JP 2001505062-A/1
PD 17-APR-2001
PF 19-FEB-1998 JP 1998536840
PR 19-FEB-1997 US 08/089882
PI MARC TESSIER LAVIGNE, DAVID E LEONARDO, LINDSAY HINCK, MASAYUKI
PI MASU,
PC C07K1/00, C07K14/00, C07K17/00, C07H21/02, C07H21/04, G01N33/53 CC
CC Topology: Linear;
FH Key Location/Qualifiers.
1..3014
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 2.1e-19 Length: 3014
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x BD057524 (1-3014)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGACTGAGTGGTCCGCTCTGCAGCGCCAGCTGTGGCGGGCTGGCAGAAACGG 795
Qy 21 SerArgSerCysThrAsnProAlaProLeuAenGlyAlaPheCysGluGlyGlnAen 40
Db 796 AGCCGGAGCTGCACCAACCGCGCCTCTCAACGGGGGGCGCTTCTGTGAGGGGGCAGAAT 855
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAACAGCCTGCCACCCTGTGTC 885

RESULT 7
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MMU487852 3992 bp mRNA linear ROD 24-SEP-2002
LOCUS Mus musculus mRNA for netrin receptor Unc5h1 (Unc5h1 gene).
DEFINITION
ACCESSION AJ487852
VERSION 1
KEYWORDS netrin receptor Unc5h1; Unc5h1 gene.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1
Engelkamp,D.
Cloning of three mouse Unc5 genes and their expression patterns at
mid-gestation
Mech. Dev. 118 (1-2), 191-197 (2002)
JOURNAL MEDLINE 2239710
PUBMED 12351186
REFERENCE 2 (bases 1 to 3992)
AUTHORS Engelkamp,D.
TITLE Direct Submission
JOURNAL Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for
Brain Research, Deutschordenstrasse 46, Frankfurt 60528, GERMANY
FEATURES
source
1. .3992
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
1. .3992
/gene="Unc5h1"
232. .2928
/gene="Unc5h1"
/codon_start=1
/product="netrin receptor Unc5h1"
/protein_id="CAD32250.1"
/db_xref="GI:22035784"
/db_xref="GOA:Q8K1S4"
/db_xref="UniProt/T/EMBL:Q8K1S4"
/translation="MAVRPGLWPAALLGLVLTWLRGSAQASATVNPVPGANPDLLP
HFLVEPDDVIVKKNPVLLVCVAPATQIFPKNGEWRVQRVDHVERSTOGSSGLPTM
EVRINVRQVQVFLGEVWCQVATQSSSGTTSKQAYIRIAYLRNFEQPLAKEV
SLEQIVLPKPPGIPPAEVEWLRNEDLVDPLDPNVIYTRHSLVVRQARLADTAN
YTCVAKNIVARRRASAIVVYVNGSWTWTEWVSCSACGSGMKRSRCTNPAPLN
GGAFCEGQVQKTCATCLCPVDGWSWPSKWSACGLDCTHWRSECSDPAPRNGREC
RGADLDRNCTDCLHTSGSPEDVALYIGLVAVAVCLILLVLLVLYCRKEGLDS
RVADSSILTSQFQVPSIKPSKADNPHLITIQDLSLTITTYTQSLCPRQGPSPFQL
SNHLLSPGLSGRHLHSSPTSEADFVSRSLSTQNYFRSLPRGTSNMYATFNFLGG
RLMIPNTGISILLIPDAIPRGIYIYTLHKPEDVRLPLAGCQTLSPIVSCGPGV
LLTPVILAMDCEGSPDSWSLRKQSCGSEMEDVHLGESPSPHLYTQLEAGAC
YVFTQGLRFPALVGEALSVATKRLRLLPAPVACTSLEYNIRVYCYLHDHDLKEVV
OLEKQGLQIQEPRVLHFVDSYHNLRLSHDVPSSLWKSLLVSYOEIPYHLWNGT
QQYLHCTFTLERNVASTSDLACKVWVQVGDGGSFNINFTKDTFRFAEMLALESG
GVPAIVGSPAPKIPFLIRQKIITSLDPPCSRGDWRTLAQKHLHDLHLSFFASKPSPT
AMILNLWEARHFPNGNLGQLAAAVAGLQPDAGLFTVSEAC"

ORIGIN
Alignment Scores:
Pred. No.: 2.82e-19 Length: 3992
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_246_295 (1-50) x MMU487852 (1-3992)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 967 TCGACGTGGACCGAGTGTTCGTGACAGTCCAGCTGTGGCGTGGCTGCACAGCG 1026
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 1027 AGCGGAGCTGCACCAACCGGCACCTCTCAACGGGGCGCGCTTCGTGTGGGGGAGCAAT 1086

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 1087 GTCCAGAAAACAGCTCGCCACTCTGTGC 1116
RESULT 8
LOCUS AK122575 4294 bp mRNA linear ROD 15-MAR-2003
DEFINITION Mus musculus mRNA for mKIAA1976 protein.
ACCESSION AK122575
VERSION AK122575.1 GI:28972881
KEYWORDS FLI_CDNA.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Aizawa,H., Yuasa,S.,
Nakajima,D., Nagase,T., Ohara,O. and Koga,H.
Prediction of the coding sequences of mouse homologues of KIAA
gene: II. The complete nucleotide sequences of 400 mouse
KIAA-homologous cDNAs identified by screening of terminal sequences
of cDNA clones randomly sampled from size-fractionated libraries
DNA Res. 10, 35-48 (2003)
2 (bases 1 to 4294)
Direct Submission
Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.
Submitted (07-FEB-2003) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)
The CREATE program supported by Japan science and technology
corporation; cDNA full insert sequencing; Kazusa DNA Research
Institute; cDNA library construction, clone selection and 5'- &
3'-end one pass sequencing.
FEATURES
Location/Qualifiers
source
1. .4294
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="mbh03993"
/tissue_type="brain"
/dev_stage="adult"
/notes="vector:modified pBC SK+"
1. .4294
/gene="mKIAA1976"
/genes="mKIAA1976"
/notes="CDS is predicted by in silico analysis. Start codon
is not identified."
/codon_start=1
/evidence="not_experimental"
/product="mKIAA1976 protein"
/protein_id="BAC65857.1"
/db_xref="GI:28972882"

ORIGIN
Alignment Scores:
Pred. No.: 3.04e-19 Length: 4294
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_246_295 (1-50) x AK122575 (1-4294)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20

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Db      734  TCGACGTGACCGAGTGGTCCGCTCTGCAGCGCCAGCTGTGGCGCGGTGGCGCAGAAACGG 793
      21  SerArgSerCysThrAsnProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAen 40
      794  AGCCGGAGCTGCACCAACCGGCACCTCTCAACGGGGGGCGCTTCTGTGAGGGGCGAGAAAT 853
      41  ValGlnLysThrAlaCysAlaThrLeuCys 50
      854  GTCCAGAAAACAGCTGCGCCACTCTGTGC 883

RESULT 9
AC027318      121282 bp  DNA  linear  PRI 01-DEC-2002
LOCUS      Homo sapiens chromosome 5 clone CTC-347K15, complete sequence.
AC027318
ACCESSION  AC027318.5  GI:25989047
VERSION
KEYWORDS  HTG.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 121282)
AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE     Direct Submission
JOURNAL   Unpublished
REFERENCE  2  (bases 1 to 121282)
AUTHORS   DOE Joint Genome Institute.
TITLE     Direct Submission
JOURNAL   Submitted (30-MAR-2000) Production Sequencing Facility, DOE Joint
           Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE  3  (bases 1 to 121282)
AUTHORS   DOE Joint Genome Institute.
TITLE     Direct Submission
JOURNAL   Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
           Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE  4  (bases 1 to 121282)
AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE     Direct Submission
JOURNAL   Submitted (01-DEC-2002) DOE Joint Genome Institute, 2800 Mitchell
           Drive, Walnut Creek, CA 94598, USA
COMMENT   On Dec 1, 2002 this sequence version replaced gi:19224786.
           Draft Sequence Produced by DOE Joint Genome Institute
           www.jgi.doe.gov
           Finishing Completed at Stanford Human Genome Center
           www.shgc.stanford.edu
           Quality: Phrap Quality >=40 99.9% of Sequence;
           Estimated Total Number of Errors is 0.1.
           NOTE: Shatter libraries failed to verify number of repeat copies
           13700-15000. Unsure number of repeat copies 13700-15000.
FEATURES             Location/Qualifiers
     source           1..121282
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTC-347K15"
     misc_feature     13700..15000
                     /note="NOTE: Shatter libraries failed to verify number of
                     repeat copies 13700-15000. Unsure number of repeat copies
                     13700-15000."
ORIGIN
Alignment Scores:
Pred. No.:          9,77e-18      Length:      121282
Score:              290.00        Matches:      50
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%   Mismatches:  0
Query Match:        100.00%     Indels:        0
DB:                  9           Gaps:          0
US-10-624-932C-2_COPY_246_295 (1-50) x AC027318 (1-121282)

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Qy      1  SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
      12403  TCGACGTGACCGAGTGGTCCGCTCTGCAGCGCCAGCTGTGGCGCGGTGGCGCAGAAACGG 12462
      21  SerArgSerCysThrAsnProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAen 40
      12463  AGCCGGAGCTGCACCAACCGGCACCTCTCAACGGGGGGCGCTTCTGTGAGGGGCGAGAAAT 12522
      41  ValGlnLysThrAlaCysAlaThrLeuCys 50
      12523  GTCCAGAAAACAGCTGCGCCACTCTGTGC 12552

RESULT 10
AC034209/c      166534 bp  DNA  linear  HTG 18-JUL-2000
LOCUS      Homo sapiens chromosome 5 clone CTC-499E20, WORKING DRAFT SEQUENCE,
           12 ordered pieces.
AC034209
ACCESSION  AC034209.3  GI:9256723
VERSION    HTG; HTGS_PHASE2; HTGS_DRAFT.
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 166534)
AUTHORS   DOE Joint Genome Institute.
TITLE     Sequencing of Human Chromosome 5
JOURNAL   Unpublished
REFERENCE  2  (bases 1 to 166534)
AUTHORS   DOE Joint Genome Institute.
TITLE     Direct Submission
JOURNAL   Submitted (05-APR-2000) Production Sequencing Facility, DOE Joint
           Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
           On Jul 18, 2000 this sequence version replaced gi:8655958.
COMMENT   -----Genome Center
           Center: Joint Genome Institute
           Center Code: JGI
           Web site: http://www.jgi.doe.gov
           -----
           Project Information
           Center Project Name: 376912
           Center clone name: CIT-HSPC_499E20
           -----
           Summary Statistics
           Consensus quality: 156088 bases at least Q40
           Consensus quality: 162568 bases at least Q30
           Consensus quality: 163999 bases at least Q20
           Estimated insert size: 169000; pulse field gel estimation
           Quality coverage: 8.94 in Q20 bases; sum-of-contigs estimation
           Quality coverage: 9.1 in Q20 bases; pulse field gel estimation
           * NOTE: This is a 'working draft' sequence. It currently
           * consists of 12 contigs. Gaps between the contigs
           * are represented as runs of N. The order of the pieces
           * is believed to be correct as given, however the sizes
           * of the gaps between them are based on estimates that have
           * been provided by the submitter.
           * This sequence will be replaced
           * by the finished sequence as soon as it is available and
           * the accession number will be preserved.
           * 1 3977: contig of 3977 bp in length
           * 3978 4077: gap of unknown length
           * 4078 8171: contig of 4094 bp in length
           * 8172 8271: gap of unknown length
           * 8272 25671: contig of 17400 bp in length
           * 25672 25771: gap of unknown length
           * 25772 41848: contig of 16077 bp in length
           * 41849 58436: contig of 16488 bp in length
           * 58437 58537: gap of unknown length
           * 58537 74135: contig of 15599 bp in length
           * 74136 74235: gap of unknown length
           * 74236 81773: contig of 7538 bp in length

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* 81774 81873: gap of unknown length
* 81874 88590: contig of 6717 bp in length
* 88591 88690: gap of unknown length
* 88691 107051: contig of 18361 bp in length
* 107052 107151: gap of unknown length
* 107152 116497: contig of 9346 bp in length
* 116498 116597: gap of unknown length
* 116598 157034: contig of 40437 bp in length
* 157035 157134: gap of unknown length
* 157135 166534: contig of 9400 bp in length.

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FEATURES

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source
1. 166534
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clones="CTC-499E20"
/clone_lib="CalTech human BAC library C"

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ORIGIN

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Alignment Scores:
Pred. No.: 1.36e-17 Length: 166534
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

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US-10-624-932C-2_COPY_246_295 (1-50) x AC034209 (1-166534)

```

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Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 52704 TCGACGTGGACCGAGTGTCTGCTGCAGCCAGCTGTGTGGCCGGCTGCAGAAACGG 52645
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 52644 AGCCGGAGCTCACCACACCGCGCTCTCAACGGGGCGCTTCTGTGAGGGGCAGAAAT 52585
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 52584 GTCCAGAAAACAGCGCTGCCACCGCTGTGC 52555

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RESULT 11

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AC012283/c AC012283 168168 bp DNA linear HTG 26-MAY-2000
DEFINITION Homo sapiens clone RP11-1G22, WORKING DRAFT SEQUENCE, 8 unordered
pieces.

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AC012283 AC012283
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 168168)
Birken, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-1G22
Unpublished
2 (bases 1 to 168168)
Birken, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
Gallagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
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Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

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TITLE
JOURNAL

COMMENT

Direct Submission
Submitted (22-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 28, 2000 this sequence version replaced gi:6094590.
All repeats were identified using RepeatMasker:
Snitt, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WTHR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2487
Center clone name: 1_G22
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 125212 bases at least Q40
Consensus quality: 145318 bases at least Q30
Consensus quality: 159522 bases at least Q20
Insert size: 170000; agarose-fp
Insert size: 167468; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
Quality coverage: 4.2 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1 1018: contig of 1018 bp in length
* 1019 1118: gap of 100 bp
* 1119 3720: contig of 2602 bp in length
* 3721 3820: gap of 100 bp
* 3821 6477: contig of 2657 bp in length
* 6478 6577: gap of 100 bp
* 6578 23880: contig of 17303 bp in length
* 23881 23980: gap of 100 bp
* 23981 47755: contig of 23775 bp in length
* 47756 47855: gap of 100 bp
* 47856 86463: contig of 38608 bp in length
* 86464 86563: gap of 100 bp
* 86564 127504: contig of 40941 bp in length
* 127505 127604: gap of 100 bp
* 127605 168168: contig of 40564 bp in length.

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FEATURES

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23981. 47755
/notes="assembly_fragment"
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/notes="assembly_fragment"

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47856. 86463
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misc_feature 127605..168168
/Note="assembly_fragment
clone_end:SP6
vector_side:left"

ORIGIN
Alignment Scores:
Pred. No.:
Score: 1.37e-17 Length: 168168
Percent Similarity: 290.00 Matches: 50
Best Local Similarity: 100.00% Conservative: 0
Query Match: 100.00% Mismatches: 0
DB: 2 Indels: 0
Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AC012283 (1-168168)

QY 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
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QY 21 SerArgSerCysThrAsnProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAsn 40
DB 162295 AGCCGGAGCTGCACCAACCGCGGCTCTCAACGGGGGCGCTTCTGTGAGGGCGCAGAT 162236

QY 41 ValGlnLysThrAlaCysAlaThrIeuCys 50
DB 162235 GTCCAGAAACAGCCTGGCGCCACCCTGTGC 162206

RESULT 12
AC139592/c 231407 bp DNA linear HTG 27-MAR-2003
LOCUS Rattus norvegicus clone CH230-12014, WORKING DRAFT SEQUENCE, 54
DEFINITION unorderd pieces.
ACCESSION AC139592
VERSION AC139592.2 GI:28269340
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 231407)
Murny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,P.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
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Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
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Lorenshewa,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J.,
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Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhiney,S., McLeod,M., McNeill,T., Meenen,B., Milosavljevic,A.,
Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,
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Newton,N., Nguyen,N., Norris,S., Nwaokemele,O., Okwuonu,G.,
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Olarnpuneagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H.,
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Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,A.,
Reaves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y.,
Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A.,
Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S.,
Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A.,
Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E.,
Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A.,
Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S.,
Tingey,A., Trejos,Z., Umani,K., Valas,R., Vera,V., Villasana,D.,
Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J.,
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Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,
Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,
Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,
Holt,R.A., Smith,H.O., Weinstein,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 231407)
Worley,K.C.
Direct Submission
Submitted (06-FEB-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 231407)
Worley,K.C.
Direct Submission
Submitted (27-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Feb 7, 2003 this sequence version replaced gi:28261442.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KDPU
Center clone name: CH230-12014
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 199497 bases at least Q40
Consensus quality: 205776 bases at least Q30
Consensus quality: 210022 bases at least Q20
Estimated insert size: 207384; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 54 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1 1011: contig of 1011 bp in length
* 1012 1111: gap of unknown length
* 1112 2158: contig of 1047 bp in length
* 2159 2258: gap of unknown length
* 2259 3347: contig of 1089 bp in length
* 3348 3447: gap of unknown length
* 3448 4572: contig of 1125 bp in length
* 4573 5908: contig of 1236 bp in length
* 5909 6008: gap of unknown length
* 6009 7270: contig of 1262 bp in length
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*	8484	8583: gap of unknown length
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*	13597	14792: contig of 1196 bp in length
*	14793	14892: gap of unknown length
*	14893	15915: contig of 1023 bp in length
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*	16016	17452: contig of 1437 bp in length
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*	19787	19886: gap of unknown length
*	19887	20918: contig of 1032 bp in length
*	20919	21018: gap of unknown length
*	21019	22399: contig of 1381 bp in length
*	22400	22499: gap of unknown length
*	22500	24283: contig of 1784 bp in length
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*	27193	28841: contig of 1649 bp in length
*	28842	28941: gap of unknown length
*	28943	31580: contig of 2639 bp in length
*	31581	31680: gap of unknown length
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*	33617	33716: gap of unknown length
*	33717	35801: contig of 2085 bp in length
*	35802	35901: gap of unknown length
*	35902	38450: contig of 2549 bp in length
*	38451	38550: gap of unknown length
*	38551	41970: contig of 3420 bp in length
*	41971	44070: gap of unknown length
*	44072	44856: contig of 2786 bp in length
*	44857	44956: gap of unknown length
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*	47193	47292: gap of unknown length
*	47293	50212: contig of 2920 bp in length
*	50213	50312: gap of unknown length
*	50313	53414: contig of 3102 bp in length
*	53415	53514: gap of unknown length
*	53515	56566: contig of 3052 bp in length
*	56567	56666: gap of unknown length
*	56667	59001: contig of 2235 bp in length
*	59002	59001: gap of unknown length
*	59002	63539: contig of 4538 bp in length
*	63540	63639: gap of unknown length
*	63640	66682: contig of 3043 bp in length
*	66683	66782: gap of unknown length
*	66783	69733: contig of 2951 bp in length
*	69734	69833: gap of unknown length
*	69834	73169: contig of 3336 bp in length
*	73170	73269: gap of unknown length
*	73270	76045: contig of 2776 bp in length
*	76046	76145: gap of unknown length
*	76146	80361: contig of 4216 bp in length
*	80362	80461: gap of unknown length
*	80462	83386: contig of 4925 bp in length
*	83387	83486: gap of unknown length
*	83487	90242: contig of 4756 bp in length
*	90243	90342: gap of unknown length
*	90343	94339: contig of 3997 bp in length
*	94340	94439: gap of unknown length
*	94440	98774: contig of 4335 bp in length
*	98775	98874: gap of unknown length
*	98875	104616: contig of 5742 bp in length
*	104617	104716: gap of unknown length
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*	109040	109139: gap of unknown length

* 109140	115555:	contig of 7416 bp in length
* 116556	116555:	gap of unknown length
* 122734	122734:	contig of 6079 bp in length
* 122834	122834:	gap of unknown length
* 122835	131928:	contig of 9094 bp in length
* 132028	132028:	gap of unknown length
* 132029	132029:	contig of 6030 bp in length
* 138059	138158:	gap of unknown length
* 138159	146320:	contig of 8162 bp in length
* 146321	146420:	gap of unknown length
* 146421	155651:	contig of 9231 bp in length

Alignment Scores:

Pred. No.:	1, 91e-17	Length:	231407
Score:	290.00	Matches:	50
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-10-624-932C-2_COPY_246_295 (11-50) x AC139592 (1-231407)

Qy	1	SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg	20
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Db	181064	AGCCGGAGCTGCACCACCCGCCACTCTCAACGGGGGGCGCTTTCTGTAGGGGGCAGAAT	181005
Qy	41	ValGlnLysThrAlaCysAlaThrLeuCys	50
Db	181004	GTCCAGAAAACAGCGCTGGCCACTCTGTGTC	180975

RESULT 13

AC123700/c

LOCUS

DEFINITION Mus musculus chromosome 13 clone RP23-335A11 map 13, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.

ACCESSION AC123700

VERSION AC123700.4 GI:45268905

KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, I., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Collangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeAtellano, K., Dewar, K., Diaz, J., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazzara, R., Landers, T., Lehoczyk, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneses, L., Minova, T., Mieng, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Ribback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topnam, K., Travers, M., Travis, N., Trigglio, J., Vasiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.M.

TITLE (Bases 1 to 242128)

JOURNAL Unpublished

REFERENCE 2 (Bases 1 to 242128)

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE
JOURNALREFERENCE
AUTHORS

Direct Submission
Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 242128)
Birren,B., Nuebaum,C., Lander,B., Abouelleil,A., Allen,N., Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collimore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A., Karatas,A., Kelle,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., MacLean,C., MacDonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Melidrim,J., Menius,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (09-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 9, 2004 this sequence version replaced gi:28933837.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

TITLE
JOURNAL

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIER
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L26431
Center clone name: 335_A_11

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 80291: contig of 80291 bp in length
* 80292 80391: gap of 100 bp
* 80392 105410: contig of 25019 bp in length
* 105411 105510: gap of 100 bp
* 105511 172522: contig of 67412 bp in length
* 172523 173022: gap of 100 bp
* 173023 182093: contig of 9071 bp in length
* 182094 182193: gap of 100 bp
* 182194 207358: contig of 25165 bp in length
* 207359 207458: gap of 100 bp
* 207459 222746: contig of 15288 bp in length
* 222747 222846: gap of 100 bp
* 222847 242128: contig of 19282 bp in length.

FEATURES
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ORIGIN

Alignment Scores:

Pred. No.: 2e-17 Length: 242128
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AC123700 (1-242128)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyATgGlyTTPGlnLysArg 20

Db 150663 TCGACGTGGACCGAGTGGCTGCTGCGAGTCCAGCTGTGGCGTGGCTGGCAGAAACGG 150604

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnhen 40

Db 150603 AGCCGGAGTGCACCAACCGGCACCTCTCAACGGGGCGCTTCTGTGAGGGGCAGAAAT 150544

Qy 41 ValGlnLysThrAlaCysAlaThrIleuCys 50

Db 150543 GTCCAGAAACAGCGCTGCCCACTCTGTGC 150514

RESULT 14

BC041156

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 2270)

1 (bases 1 to 2270)

1 (bases 1 to 2270)

1 (bases 1 to 2270)

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Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteaman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 84 Row: d Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16933524.

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RESULT 15

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LOCUS CQ881064 2612 bp DNA linear PAT 11-OCT-2004
DEFINITION Sequence 13 from Patent WO2004083371.
ACCESSION CQ881064
VERSION CQ881064.1 GI:54034173
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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REFERENCE

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1. Dahl, N.
AUTHORS
TITLE Genes associated with obesity and methods for using the same
JOURNAL Patent: WO 2004083371-A 13 30-SEP-2004;
Astrazeneca AB (SE)
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1. .2612
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Query Match: 85.86% Indels: 0
DB: 6 Gaps: 0
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Search completed: September 9, 2005, 09:41:08
Job time : 2156.73 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 20:54:46 ; Search time 258.585 Seconds
(without alignments)
1144.643 Million cell updates/sec

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Perfect score: 290

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	290	100.0	2697	6 AAK52891	AAK52891 Human net
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7	290	100.0	2907	4 AAK52261	AAK52261 Human pol
8	290	100.0	3014	2 AAV52940	AAV52940 Rat UNC-5
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10	249	85.9	2780	13 ADR99251	Adr99251 Human sRO
11	249	85.9	2796	10 AAL56266	AAL56266 Human thr
12	249	85.9	2986	13 ADR99249	Adr99249 Human IRO
13	249	85.9	3646	5 AAS75738	AAS75738 DNA encod
14	249	85.9	3646	13 ADR99257	Adr99257 Human unc
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16	243	83.8	2880	12 ADH71633	Adh71633 Human gen
17	243	83.8	2881	6 ABK49422	ABK49422 DNA encod
18	243	83.8	2881	10 ADG42568	ADG42568 Novel hum
19	243	83.8	2881	12 ADH71649	Adh71649 Human gen
20	243	83.8	2881	12 ADH71635	Adh71635 Human gen
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36	239	82.4	2661	10 ADC77421	Adc77421 Human tra
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ALIGNMENTS

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DT 25-MAR-2004 (first entry)
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XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nontropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
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PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
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PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
(CURA-) CURAGEN CORP.

XX
PI Alsobrook JP, Alvarez E, Anderson DW, Boldog EL, Casman SJ, Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K; Etenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X; Gusev VY, Herrmann JM, Ji W, Kekuda R, Li L, Liu X, Macdougall JR; MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS; Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L; Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA; Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M; Zhong H;
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71620.
XX
PI New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX Example 21; SEQ ID NO 515; 1880pp; English.
XX The invention relates to a novel isolated polypeptide (NOVX). A polypeptide of the invention has cytostatic, immunomodulator, neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and antilipemic activity, and may have a use in gene therapy, and as a vaccine. The polypeptides are encoded by NOVX polynucleotides comprising any of the 303 fully defined nucleotide sequences given in the specification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide, polynucleotide and antibody are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cancer, cachexia, Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence encodes a NOVX polypeptide of the invention.
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Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Db 727 AGCGGAGCTGCACCAACCGCGCCCTCTCAACGCGGCGCGCTTCTGTGAGGGCGCAGAA 786
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RESULT 2
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AC ADH71613;
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DT 25-MAR-2004 (first entry)
XX Human gene of the invention NOV21c SEQ ID NO:509.
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic; anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy; vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;

obesity; diabetes; infectious disease; metabolic syndrome X; dyslipidaemia.

Homo sapiens.

WO2003102155-A2.

11-DEC-2003.

03-JUN-2003; 2003WO-US017430.

03-JUN-2002; 2002US-0385120P.

04-JUN-2002; 2002US-038784P.

05-JUN-2002; 2002US-0386041P.

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06-JUN-2002; 2002US-0386376P.

06-JUN-2002; 2002US-0386453P.

06-JUN-2002; 2002US-0386864P.

06-JUN-2002; 2002US-0387016P.

07-JUN-2002; 2002US-0386796P.

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14-JUN-2002; 2002US-0389120P.

KW obesity; diabetes; infectious disease; metabolic syndrome X; dyslipidaemia.

XX Homo sapiens.

OS WO2003102155-A2.

PN 11-DEC-2003.

XX 03-JUN-2003; 2003WO-US017430.

XX 03-JUN-2002; 2002US-0385120P.

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PR 14-JUN-2002; 2002US-0389120P.

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PR 14-JUN-2002; 2002US-0389146P.

PR 17-JUN-2002; 2002US-0389729P.

PR 17-JUN-2002; 2002US-0389742P.

PR 18-JUN-2002; 2002US-0389884P.

PR 19-JUN-2002; 2002US-0390006P.

PR 19-JUN-2002; 2002US-0390209P.

PR 21-JUN-2002; 2002US-0390763P.

PR 17-JUL-2002; 2002US-0396708P.

PR 06-AUG-2002; 2002US-0401628P.

PR 09-AUG-2002; 2002US-0402156P.

PR 09-AUG-2002; 2002US-0402256P.

PR 09-AUG-2002; 2002US-0402389P.

PR 12-AUG-2002; 2002US-0402786P.

PR 12-AUG-2002; 2002US-0402816P.

PR 12-AUG-2002; 2002US-0402821P.

PR 12-AUG-2002; 2002US-0402821P.

PR 13-AUG-2002; 2002US-0403448P.

PR 13-AUG-2002; 2002US-0403459P.

PR 13-AUG-2002; 2002US-0403531P.

PR 13-AUG-2002; 2002US-0403532P.

PR 13-AUG-2002; 2002US-0403563P.

PR 13-AUG-2002; 2002US-0406317P.

PR 15-AUG-2002; 2002US-0403617P.

PR 26-AUG-2002; 2002US-0406182P.

PR 26-AUG-2002; 2002US-0406355P.

PR 27-AUG-2002; 2002US-0406240P.

PR 12-SEP-2002; 2002US-0410084P.

PR 20-SEP-2002; 2002US-0412528P.

PR 23-SEP-2002; 2002US-0412731P.

PR 30-SEP-2002; 2002US-0414801P.

PR 30-SEP-2002; 2002US-0414839P.

PR 30-SEP-2002; 2002US-0414840P.

PR 30-SEP-2002; 2002US-0414954P.

PR 09-OCT-2002; 2002US-0417186P.

PR 09-OCT-2002; 2002US-0417406P.

PR 23-OCT-2002; 2002US-0420639P.

PR 28-OCT-2002; 2002US-0421156P.

PR 31-OCT-2002; 2002US-0422690P.

PR 01-NOV-2002; 2002US-0423130P.

PR 05-NOV-2002; 2002US-00423798.

PR 05-NOV-2002; 2002US-0423798P.

PR 12-NOV-2002; 2002US-0425453P.

XX (CURA-) CURAGEN CORP.

XX

XX Alsebrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ, Catterton E, Chapoval A, Crabtree-Bokor JK, Edinger SR, Ellerman K, Ettenberg S, Gargolli EA, Gerlach VL, Gorman L, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR, Maclachlan T, Malyankar UM, Mexick AJ, Millet I, Mishra VS, Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L, Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA, Smithson G, Spytek KA, Stone DJ, Vernhet CAM, Voss EZ, Zhong M, Zhong H;

DR WPI; 2004-081935/08.

DR P-PSDB; ADH71614.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

PT

XX Example 21; SEQ ID NO 509; 1880pp; English.

XX

CC The invention relates to a novel isolated polypeptide (NOVX). A polypeptide of the invention has cytostatic, immunomodulator, neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and antilipemic activity, and may have a use in gene therapy, and as a vaccine. The polypeptides are encoded by NOVX polynucleotides comprising any of the 303 fully defined nucleotide sequences given in the specification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide, polynucleotide and antibody are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cancer, cachexia, Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence encodes a NOVX polypeptide of the invention.

XX

SQ Sequence 1009 BP; 195 A; 314 C; 336 G; 164 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.28e-21	Length:	1009
Score:	290.00	Matches:	50
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-624-932C-2_COPY_246_295 (1-50) x ADH71613 (1-1009)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyAcGlyTrpGlnIysArg 20

Db 671 TCGACGTGGACCGAGTGGTCCGTCGACGCCAGCTGGGCGCGCTGGCGAAGCG 730

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40

Db 731 AGCCGGAGCTGCACCAACCCCGCGCTCTCAACGGGGGCGCTTCTGTGTGGGGGAGAT 790

Qy 41 ValGlnLysThrAlaCysAlaThrIleuCys 50

CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
 CC of the invention is useful for detecting a coding sequence for the UNC5H-
 CC 1 protein. The present sequence represents a DNA sequence encoding the
 CC human netrin binding membrane receptor UNC5H-1 protein of the invention
 XX
 SQ Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4.12e-21 Length: 2697
 Score: 290.00 Matches: 50
 Percent Similarity: 100.00% Conservations: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x ABK52891 (1-2697)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
 Db 736 TCGACGTGGACCGAGTGGTCCGTCTGCAGCCGACGCTGTGGCGCGGTGCAGAAACGG 795
 Qy 21 SerArgSerCysThrAspProAlaProLeuAenGlyGlyAlaPheCysGluGlyClnAen 40
 Db 796 AGCCGAGCTGCACCCACCCGCGCTCTCAACGGGGGCGCTTCTGTGAGGGGCGAGAT 855
 Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
 Db 856 GTCCAGAAAACAGCTGCGCCACCTGTGTC 885

RESULT 5

ABK37922
 ID ABK37922 standard; cDNA; 2752 BP.

AC ABK37922;

DT 21-MAY-2002 (first entry)

XX cDNA encoding Human protein NOV1.

XX Human; NOVX; ss; gene; cardiomyopathy; atherosclerosis; diabetes;
 KW cell signal processing disorder; metabolic disorder; obesity; infection;
 KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
 KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
 KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
 KW psychosis; neurological disorder; anxiety; schizophrenia;
 KW manic depression; dementia; dyskinesia; Huntington's disease;
 KW Gilles de la Tourette's syndrome; gene therapy.

XX Homo sapiens.

XX WO200210216-A2.

XX 07-FEB-2002.

XX 30-JUL-2001; 2001WO-US024225.

XX 28-JUL-2000; 2000US-0221409P.

XX 04-AUG-2000; 2000US-0222840P.

XX 04-AUG-2000; 2000US-0223752P.

XX 04-AUG-2000; 2000US-0223762P.

XX 04-AUG-2000; 2000US-0223769P.

XX 04-AUG-2000; 2000US-0223770P.

XX 14-AUG-2000; 2000US-0225146P.

XX 15-AUG-2000; 2000US-0225392P.

XX 15-AUG-2000; 2000US-0225470P.

XX 16-AUG-2000; 2000US-0225697P.

XX 01-FEB-2001; 2001US-0263662P.

XX 05-APR-2001; 2001US-0281645P.

XX (CURA-) CURAGEN CORP.

PA

PI Padigaru M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;
 PI Alsobrook JP, Lopley DM, Gerlach VL, Macdougall JR, Smithson G;
 XX WPI; 2002-180074/23.
 DR P-PSDB; AU85403.
 XX

PT New isolated cytoplasmic, nuclear, membrane bound, or secreted
 PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
 PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
 XX immune disorders.

PS Claim 9; Page 9-10; 213pp; English.

CC The invention relates to an isolated cytoplasmic, nuclear, membrane
 CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
 CC form. Also included are the nucleic acids encoding the NOVX proteins, a
 CC vector comprising the nucleic acid, a cell comprising the vector, an anti
 CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
 CC antibody are useful for treating or preventing a NOVX-associated
 CC disorder, where the disorder is selected from cardiomyopathy,
 CC atherosclerosis, diabetes, a disorder related to cell signal processing
 CC and metabolic pathway modulation, metabolic disorders, obesity,
 CC infectious disease, anorexia, cancer-associated cachexia, cancer,
 CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
 CC immune disorders, haematopoietic disorders, and the various
 CC dyslipidaemias, metabolic disturbances associated with obesity, the
 CC metabolic syndrome X and wasting disorders associated with chronic
 CC diseases, bacterial, fungal, protozoal and viral infections, pain,
 CC bulimia, asthma, hypertension, urinary retention, osteoporosis, angina
 CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
 CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
 CC hypertrophy, and psychotic and neurological disorders, including anxiety,
 CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
 CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
 CC nucleic acid is useful in gene therapy. The present sequence encodes a
 CC NOVX protein

SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.22e-21 Length: 2752
 Score: 290.00 Matches: 50
 Percent Similarity: 100.00% Conservations: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x ABK37922 (1-2752)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
 Db 781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCCGACGCTGTGGCGCGGTGCAGAAACGG 840

Qy 21 SerArgSerCysThrAspProAlaProLeuAenGlyGlyAlaPheCysGluGlyClnAen 40
 Db 841 AGCCGAGCTGCACCAACCCGCGCTCTCAACGGGGGCGCTTCTGTGAGGGGCGAGAT 900

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50

Db 901 GTCCAGAAAACAGCTGCGCCACCTGTGTC 930

RESULT 6

ADH71617

ID ADH71617 standard; DNA; 2752 BP.

XX ADH71617;

XX 25-MAR-2004 (first entry)

XX Human gene of the invention NOV21e SEQ ID NO:513.

XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
 KW anorectic; antidiabetic; antimicrobial; gene therapy;

KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX Homo sapiens.

XX WO2003102155-A2.

XX 11-DEC-2003.

XX 03-JUN-2003; 2003WO-US017430.

XX 03-JUN-2002; 2002US-0385120P.

XX 04-JUN-2002; 2002US-0385784P.

XX 05-JUN-2002; 2002US-0386041P.

XX 06-JUN-2002; 2002US-0386376P.

XX 06-JUN-2002; 2002US-0386453P.

XX 06-JUN-2002; 2002US-0386864P.

XX 07-JUN-2002; 2002US-0387016P.

XX 07-JUN-2002; 2002US-0386816P.

XX 07-JUN-2002; 2002US-0386931P.

XX 07-JUN-2002; 2002US-0386942P.

XX 07-JUN-2002; 2002US-0386971P.

XX 08-JUN-2002; 2002US-0387262P.

XX 10-JUN-2002; 2002US-0236960P.

XX 10-JUN-2002; 2002US-0387400P.

XX 10-JUN-2002; 2002US-0387535P.

XX 11-JUN-2002; 2002US-0387610P.

XX 11-JUN-2002; 2002US-0387625P.

XX 11-JUN-2002; 2002US-0387634P.

XX 11-JUN-2002; 2002US-0387688P.

XX 11-JUN-2002; 2002US-0387696P.

XX 11-JUN-2002; 2002US-0387702P.

XX 11-JUN-2002; 2002US-0387836P.

XX 12-JUN-2002; 2002US-0387859P.

XX 12-JUN-2002; 2002US-0387933P.

XX 12-JUN-2002; 2002US-0387934P.

XX 12-JUN-2002; 2002US-0387960P.

XX 12-JUN-2002; 2002US-0388022P.

XX 12-JUN-2002; 2002US-0388096P.

XX 13-JUN-2002; 2002US-0389123P.

XX 14-JUN-2002; 2002US-0389118P.

XX 14-JUN-2002; 2002US-0389120P.

XX 14-JUN-2002; 2002US-0389144P.

XX 17-JUN-2002; 2002US-0389146P.

XX 17-JUN-2002; 2002US-0389729P.

XX 18-JUN-2002; 2002US-0389884P.

XX 19-JUN-2002; 2002US-0390066P.

XX 21-JUN-2002; 2002US-0390209P.

XX 17-JUL-2002; 2002US-0396706P.

XX 06-AUG-2002; 2002US-0401628P.

XX 09-AUG-2002; 2002US-0402156P.

XX 09-AUG-2002; 2002US-0402256P.

XX 09-AUG-2002; 2002US-0402389P.

XX 12-AUG-2002; 2002US-0402786P.

XX 12-AUG-2002; 2002US-0402816P.

XX 12-AUG-2002; 2002US-0402821P.

XX 12-AUG-2002; 2002US-0402832P.

XX 13-AUG-2002; 2002US-0403448P.

XX 13-AUG-2002; 2002US-0403459P.

XX 13-AUG-2002; 2002US-0403531P.

XX 13-AUG-2002; 2002US-0403532P.

XX 13-AUG-2002; 2002US-0403563P.

XX 15-AUG-2002; 2002US-0406317P.

XX 26-AUG-2002; 2002US-0406182P.

XX 26-AUG-2002; 2002US-0406355P.

XX 27-AUG-2002; 2002US-0406240P.

XX 12-SEP-2002; 2002US-0410084P.

PR 20-SEP-2002; 2002US-0412528P.

PR 23-SEP-2002; 2002US-0412731P.

PR 30-SEP-2002; 2002US-0414801P.

PR 30-SEP-2002; 2002US-0414839P.

PR 30-SEP-2002; 2002US-0414840P.

PR 30-SEP-2002; 2002US-0414954P.

PR 09-OCT-2002; 2002US-0417186P.

PR 09-OCT-2002; 2002US-0417406P.

PR 23-OCT-2002; 2002US-0420639P.

PR 28-OCT-2002; 2002US-0421156P.

PR 31-OCT-2002; 2002US-0422690P.

PR 01-NOV-2002; 2002US-0423130P.

PR 05-NOV-2002; 2002US-00423798.

PR 05-NOV-2002; 2002US-0423798P.

PR 12-NOV-2002; 2002US-0425453P.

XX (CURA-) CURAGEN CORP.

XX Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;

XX Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;

XX Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;

XX Gusev VI, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;

XX MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;

XX Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;

XX Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;

XX Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;

XX Zhong H;

XX WPI; 2004-081935/08.

DR P-PSDB; ADH71618.

XX New NOVX polypeptides and nucleic acid molecules useful for preventing or

XX treating NOVX-associated disorders, e.g. cancer, diabetes, infection or

XX obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX Example 21; SEQ ID NO 513; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A

XX polypeptide of the invention has cytostatic, immunomodulator,

XX neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and

XX antitiphaemic activity, and may have a use in gene therapy, and as a

XX vaccine. The polypeptides are encoded by NOVX polynucleotides comprising

XX any of the 303 fully defined nucleotide sequences given in the

XX specification. The polypeptide is useful in the manufacture of a

XX medicament for treating a syndrome associated with a human disease. The

XX polypeptide, polynucleotide and antibody are useful in diagnosing. The

XX treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,

XX Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious

XX diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are

XX further used as hybridisation probes, in chromosome mapping, tissue

XX typing, preventive medicine, and pharmacogenomics. The present sequence

XX encodes a NOVX polypeptide of the invention.

XX SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:

Pred No.: 4.22e-21 Length: 2752

Score: 290.00 Matches: 50

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 12 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x ADH71617 (1-2752)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnIysArg 20

Db 781 TCGACGTGGACCGAGTGGTCCGCTGTGACGCCAGCTGTGGCGCGGTGCAGAACGG 840

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40

Db 841 AGCCGGAGCTGCACCAACCCGCGCCCTCTCACGGGGGCGCTTTTCTGTGGGGGCGAGT 900

QY 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
 DB 901 GTCCAGAAAAACAGCCTGGCGCCACCCTGTGC 930

RESULT 7
 AAK52261
 ID AAK52261 standard; cDNA; 2907 BP.
 XX AAK52261;
 AC
 XX 06-NOV-2001 (first entry)
 DT
 XX Human polynucleotide SEQ ID NO 806.
 DE
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200157190-A2.
 PN
 XX 09-AUG-2001.
 FD
 XX 05-FEB-2001; 2001WO-US004098.
 PP
 XX 03-FEB-2000; 2000US-00496914.
 PR
 XX 27-APR-2000; 2000US-00560875.
 PR
 XX 20-JUN-2000; 2000US-00598075.
 PR
 XX 19-JUL-2000; 2000US-00620325.
 PR
 XX 01-SEP-2000; 2000US-00654936.
 PR
 XX 15-SEP-2000; 2000US-00663561.
 PR
 XX 20-OCT-2000; 2000US-00693325.
 PR
 XX 30-NOV-2000; 2000US-00728422.
 XX
 FA (HYSEQ-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 XX WPI; 2001-476283/51.
 DR P-PSDB; AAM79128.
 XX
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 XX
 XX Claim 1; Page 2691-2694; 6221pp; English.
 XX
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3566 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 XX Sequence 2907 BP; 552 A; 966 C; 881 G; 508 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 4, 51e-21 Length: 2907
 Score: 290.00 Matches: 50
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-624-932c-2_COPY_246_295 (1-50) x AAK52261 (1-2907)

QY 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
 DB 946 TCGACGTGGACCGAGGTGCTGTGACGCCACCTGTGGCGCGCTGGCAGAACGG 1005

QY 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
 DB 1006 AGCCGGAGCTGCACCAACCCGGCGCTCTCAACGGGGCGCTTCTGTGAGGGGAGAAT 1065

QY 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
 DB 1066 GTCCAGAAAAACAGCCTGGCGCCACCCTGTGC 1095

RESULT 8
 AAV52940
 ID AAV52940 standard; cDNA; 3014 BP.
 XX AAV52940;
 AC
 XX 25-MAR-2003 (revised)
 DT 21-DEC-1998 (first entry)
 XX
 DE Rat UNC-5 homologue unc5h-1 cDNA.
 KW UNC-5; UNC5H-1; rat; netrin receptor; cell migration; axon guidance;
 KW diagnosis; therapy; ds.
 XX
 OS Rattus sp.
 XX
 XX Key Location/Qualifiers
 XX CDS 1..2697
 XX /*tag= a
 XX
 XX WO9837085-A1.
 XX
 XX 27-AUG-1998.
 XX
 XX 19-FEB-1998; 98WO-US003143.
 XX
 XX 19-FEB-1997; 97US-00808982.
 XX
 XX (REGC) UNIV CALIFORNIA.
 XX
 XX Tessier-Lavigne M, Leonardo ED, Hinck L, Masu M, Keino-Masu K;
 PI
 XX WPI; 1998-495364/42.
 DR P-PSDB; AAW78898.
 XX
 XX Netrin-binding, vertebrate proteins - useful for diagnosis, therapy and
 PT the biopharmaceutical industry.
 XX
 XX Claim 7; Page 15-17; 32pp; English.
 XX
 XX This cDNA, termed unc5h-1, comprises a rat homologue of Caenorhabditis
 CC elegans unc-5. Rat unc5h-1 and unc5h-2 (see AAV52942) cDNAs were isolated
 CC from an E18 brain cDNA library. The predicted proteins (see AAW78898 and
 CC AAW78900) show similarity with UNC-5. They are predicted to be involved
 CC in cell migration and axon guidance, and are characterised as receptor
 CC proteins for netrin. Gene expression is observed in regions where
 CC differentiating neurons are undergoing axogenesis. Human unc5h-1 (see
 CC AAV52941) and unc5h-2 (see AAV52943) cDNAs are also claimed. Vertebrate
 CC UNC-5 proteins may be produced recombinantly from transfected host cells
 CC by utilising these vertebrate UNC-5 nucleic acids. The invention also
 CC provides unc-5 hybridisation probes and primers, vertebrate UNC-5-
 CC specific binding agents such as specific antibodies, and methods of
 CC making and using the subject compositions in diagnosis (e.g. genetic
 CC hybridisation screens for vertebrate unc-5 transcripts), therapy (e.g.
 CC gene therapy to modulate vertebrate unc-5 gene expression) and in the
 CC biopharmaceutical industry (e.g. as immunogens, reagents for modulating
 CC cell guidance, reagents for screening chemical libraries for lead
 CC pharmacological agents, etc.). (Updated on 25-MAR-2003 to correct PI


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CC field.)
XX Sequence 3014 BP; 596 A; 977 C; 849 G; 592 T; 0 U; 0 Other;
SQ Alignment Scores:
Pred. No.: 4.7e-21 Length: 3014
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AAV52940 (1-3014)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGAGTGGTCCGCTGTCAGCCGCCAGCTGTGGCGTGGTGGCAGAAACGG 795
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCCGAGCTGCACCAACCCGGACCTCTCAACGGGGCGCCCTTCTGTGAGGGGCAGAAAT 855
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAAACAGCTGCGCCACTCTGTGC 885

RESULT 9
ADR99261
ID ADR99261 standard; cDNA; 2612 BP.
XX
AC ADR99261;
XX
DT 16-DEC-2004 (first entry)
XX
DE Splice variant human uncoordinated 5C (sUNC5C) protein encoding cDNA.
XX
KW RAR-like orphan receptor alpha 1-uncoordinated 5C; ROR-alpha-1-UNC5C;
KW ROR-alpha-5; obesity; susceptibility; anorectic; antilipaeamic;
KW antiarteriosclerotic; hepatotropic; hypotensive; antidiabetic; cardiant;
KW vasotropic; osteopathic; antiarthritic; cycostatic; gene therapy;
KW hyperlipidaemia; gene; human; ss; sUNC5C.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 1..1911
FT FT /*tag= a
FT FT /product= "Alternative splice version of human
FT FT uncoordinated 5C (UNC5C) protein"
XX
PN WO2004083371-A2.
XX
XX 30-SEP-2004.
XX
XX 16-MAR-2004; 2004WO-GB001124.
XX
XX 19-MAR-2003; 2003GB-00006185.
XX
XX (ASTR ) ASTRAZENECA AB.
XX (ASTR ) ASTRAZENECA UK LTD.
XX
XX Dahl N;
XX
XX WPI; 2004-691032/67.
XX P-ESDB; ADR99262.
XX
XX New isolated nucleic acid molecule encoding a RAR-like orphan receptor
XX alpha 1-uncoordinated 5C (RORapproximate1al-UNC5C) polypeptide, useful
XX in diagnosing or treating obesity and hyperlipidemia.
XX
XX Disclosure; SEQ ID NO 13; 96pp; English.
XX
XX The invention relates to a novel isolated nucleic acid molecule,
CC

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```

CC comprising a nucleotide sequence having at least 65% identity to a
CC degenerate variant of a fully defined sequence of 2986, 2780 or 1821 bp
CC (ADR99249, ADR99251 or ADR99255), or the complement of nucleotide
CC sequence with ADR99249, ADR99251 or ADR99255. The invention further
CC comprises: an isolated nucleic acid molecule encoding a RAR-like orphan
CC receptor alpha 1-uncoordinated 5C (ROR-alpha-1-UNC5C) polypeptide; an
CC isolated nucleic acid molecule encoding a ROR-alpha-5 polypeptide; a
CC vector comprising any of the nucleic acid molecules as cited; a host cell
CC comprising the vector; a purified fusion polypeptide of the ROR-alpha-1-
CC UNC5C polypeptide; a purified polypeptide of the ROR-alpha-5 polypeptide;
CC a method for producing a protein comprising culturing the host cell; a
CC method for detecting a polynucleotide which encodes a ROR-alpha-1-UNC5C
CC protein; a method for detecting the presence of an obesity susceptibility
CC gene; a method for detecting the presence of a translocation junction
CC between chromosome 4 at cytoband 4q 22.3 and chromosome 15 at cytoband
CC 15q22.2; a method for identifying a test compound that modulates the
CC expression of an obesity susceptibility gene identified in said method; a
CC method for identifying a test compound that modulates the activity of an
CC obesity protein encoded by the obesity susceptibility gene identified in
CC said method; a method for treating a subject having obesity; a
CC pharmaceutical composition comprising a compound identified in the
CC previous methods, and an adjuvant, diluent or carrier; making a
CC pharmaceutical composition; a method for determining if an obesity
CC susceptibility gene identified in the appropriate method; and a method
CC for diagnosing obesity, or a susceptibility to it in a subject. The
CC isolated nucleic acid molecules and compounds of the invention have the
CC following activities: anorectic, antilipaeamic, antiarteriosclerotic,
CC hepatotropic, hypotensive, antidiabetic, cardiant, vasotropic,
CC osteopathic, antiarthritic, and cycostatic. The isolated nucleic acid
CC molecules and compounds may be used in gene therapy. The compound
CC modulating the activity of an obesity protein or the expression of an
CC obesity susceptibility gene is useful in the preparation of a medicament
CC for the treatment of obesity. The compound is also useful in treating or
CC diagnosing hyperlipidaemia, and the consequences of obesity, such as
CC arteriosclerosis, fatty liver, hypertension, diabetes, coronary heart
CC disease, stroke, gallbladder disease, osteoarthritis and cancer. This
CC polynucleotide sequence represents the gene encoding the alternative
CC splice version of the human uncoordinated 5C (UNC5C) protein of the
CC invention.
XX
SQ Sequence 2612 BP; 666 A; 675 C; 674 G; 597 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.57e-17 Length: 2612
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservativity: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 13 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x ADR99261 (1-2612)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 790 TCCACCTGGACGGAGTGGTCTGTGTGAACAGCCCGCTGTGGACGAGGGGTATCAGAAACGT 849
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 850 ACAAGGACCTGTACCAACCCGGCACCCTCAATGGGGTGCCTTCTGTGAAGGCGCAGAGT 909
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 910 GTGCAGAAAATAGCTGTGACTACGTTATGC 939

RESULT 10
ADR99251
ID ADR99251 standard; cDNA; 2780 BP.
XX
XX ADR99251;
XX
XX 16-DEC-2004 (first entry)
XX
XX Human sROR-alpha-1-UNC5C protein encoding cDNA.
CC

```


XX RAR-like orphan receptor alpha 1-uncoordinated 5C; ROR-alpha-1-UNC5C;
KW ROR-alpha-5; obesity; susceptibility; anorectic; antilipemic;
KW antiarteriosclerotic; hepatotropic; hypotensive; antidiabetic; cardiac;
KW vasotropic; osteopathic; antiarthritic; cytostatic; gene therapy;
KW hyperlipidaemia; gene; human; sROR-alpha-1-UNC5C; ss.
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT 70..2079
FT CDS /*tag= a
FT /product= "Human sROR-alpha-1-UNC5C protein"
XX
XX WO2004083371-A2.
XX
XX 30-SEP-2004.
XX
XX 16-MAR-2004; 2004WO-GB001124.
XX
XX 19-MAR-2003; 2003GB-00006185.
XX (ASTR) ASTRAZENECA AB.
XX (ASTR) ASTRAZENECA UK LTD.
XX
XX Dahl N;
PI
PI WPI; 2004-691032/67.
DR P-PSDB; ADR99252.
DR
XX
XX New isolated nucleic acid molecule encoding a RAR-like orphan receptor
FT alpha 1-uncoordinated 5C (RORapproximate) polypeptide, useful
PT in diagnosing or treating obesity and hyperlipidemia.
FT
XX
XX Claim 2; SEQ ID NO 3; 96pp; English.
XX
XX The invention relates to a novel isolated nucleic acid molecule,
CC comprising a nucleotide sequence having at least 65% identity to a
CC degenerate variant of a fully defined sequence of 2986, 2780 or 1821 bp
CC (ADR99249, ADR99251 or ADR99255), or the complement of nucleotide
CC sequence with ADR99249, ADR99251 or ADR99255. The invention further
CC comprises: an isolated nucleic acid molecule encoding a RAR-like orphan
CC receptor alpha 1-uncoordinated 5C (ROR-alpha-1-UNC5C) polypeptide; an
CC isolated nucleic acid molecule encoding a ROR-alpha-5 polypeptide; a
CC vector comprising any of the nucleic acid molecules as cited; a host cell
CC comprising the vector; a purified fusion polypeptide of the ROR-alpha-1-
CC UNC5C polypeptide; a purified polypeptide of the ROR-alpha-5 polypeptide;
CC a method for producing a protein comprising culturing the host cell; a
CC method for detecting a polynucleotide which encodes a ROR-alpha-1-UNC5C
CC protein; a method for detecting the presence of an obesity susceptibility
CC gene; a method for detecting the presence of a translocation junction
CC between chromosome 4 at cytoband 4q 22.3 and chromosome 15 at cytoband
CC 15q22.2; a method for identifying a test compound that modulates the
CC expression of an obesity susceptibility gene identified in said method; a
CC method for identifying a test compound that modulates the activity of an
CC obesity protein encoded by the obesity susceptibility gene identified in
CC said method; a method for treating a subject having obesity; a
CC pharmaceutical composition comprising a compound identified in the
CC previous methods, and an adjuvant, diluent or carrier; making a
CC pharmaceutical composition; a method for determining if an obesity
CC susceptibility gene identified in the appropriate method; and a method
CC for diagnosing obesity, or a susceptibility to it in a subject. The
CC isolated nucleic acid molecules and compounds of the invention have the
CC following activities: anorectic, antilipemic, antiarteriosclerotic,
CC hepatotropic, hypotensive, antidiabetic, cardiac, vasotropic,
CC osteopathic, antiarthritic, and cytostatic. The isolated nucleic acid
CC molecules and compounds may be used in gene therapy. The compound
CC modulating the activity of an obesity protein or the expression of an
CC obesity susceptibility gene is useful in the preparation of a medicament
CC for the treatment of obesity. The compound is also useful in treating or
CC diagnosing hyperlipidaemia, and the consequences of obesity, such as
CC arteriosclerosis, fatty liver, hypertension, diabetes, coronary heart
CC disease, stroke, gallbladder disease, osteoarthritis and cancer. This

CC polynucleotide sequence represents the gene encoding the human sROR-alpha
CC -1-UNC5C protein of the invention.
XX
SQ Sequence 2780 BP; 721 A; 727 C; 712 G; 620 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.03e-16 Length: 2780
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 13 Gaps: 0
US-10-624-932C-2_COPY_246_295 (1-50) x ADR99251 (1-2780)
Qy 1 SerThrTrpThrGluTyrSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 901 TCCACCTGGACGGAGTGGTCTGTGTGTAAACAGCCCTGTGGACGAGGTATCAGAAAGT 960
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 961 ACAAGGAGCTTGTACCAACCCCGCACCACTCAATGGGGTGGCTTCTGTGAAGGGCAGAGT 1020
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 1021 GTGCAGAAATAGCCTGTACTACCTTATGC 1050
RESULT 11
AAL56266
ID AAL56266 standard; DNA; 2796 BP.
XX
AC AAL56266;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human thrombospondin coding sequence.
XX
KW Vector; rAAV; recombinant adeno-associated viral vector;
KW anti-angiogenesis; PEDF; angiogenesis; eye disorder; blindness;
KW retinal degeneration; macular degeneration; neovascularisation;
KW ophthalmological; gene; ds.
XX
OS Homo sapiens.
XX
XX WO2003080648-A2.
XX
XX 02-OCT-2003.
XX
XX 20-MAR-2003; 2003WO-US008667.
XX
XX 20-MAR-2002; 2002US-0366114P.
XX (UYFL) UNIV FLORIDA RES FOUND INC.
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Hauswirth WW, Campochiaro PA, Berns KI;
XX WPI; 2003-779243/73.
XX P-PSDB; ABU64297.
XX
XX Novel adeno-associated viral vector comprising polynucleotide encoding
PT pigment epithelium-derived factor, useful for treating choroidal
PT neovascularization, blindness, loss of vision.
XX
XX Claim 19; Page 44-45; Opp; English.
XX
XX The present invention relates to an adeno-associated viral (AAV) vector
CC comprising a polynucleotide that comprises a nucleic acid segment that
CC encodes a choroidal or ocular neovascularisation inhibitory polypeptide
CC operably linked to a promoter that expresses the segment to produce the
CC polypeptide in a selected mammalian host cell. Such a vector is useful
CC for providing a choroidal or ocular neovascularisation inhibitory
CC polypeptide to a mammal, for use in the therapy of ocular

```
CC neovascularisation, choroidal neovascularisation, retinal
CC neovascularisation, age-related macular degeneration, visual impairment,
CC ocular dysfunction, loss of vision, retinopathy, or blindness in a human.
CC The present sequence is a gene shown in the exemplification of the
CC invention
XX
SQ Sequence 2796 BP; 708 A; 734 C; 726 G; 628 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.04e-16 Length: 2796
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AAL56266 (1-2796)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 790 TCCACCTGGACGGAGTGTCTGTGTGTACAGCCGCTGTGGACGAGGTATCAGAAACGT 849
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 850 ACAAGGACTTGTACCAACCGGCACCACTCAATGGGGTGCCTTCTGTGAAGGCGCAGAGT 909
Qy 41 ValGlnLysThrAlaCysAlaThrIleuCys 50
Db 910 GTGCAGAAATAGCCTGTACTACGTTATGC 939

RESULT 12
ID ADR99249 standard; cDNA; 2986 BP.
AC ADR99249;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human lROR-alpha-1-UNC5C protein encoding cDNA.
XX
KW RAR-like orphan receptor alpha 1-uncordinated 5C; ROR-alpha-1-UNC5C;
KW ROR-alpha-5; obesity; susceptibility; anorectic; antilipaeamic;
KW antiarteriosclerotic; hepatotropic; hypotensive; antidiabetic; cardiant;
KW vasotrophic; osteopathic; antiarthritic; cyostatic; gene therapy;
KW hyperlipidaemia; Gene; human; lROR-alpha-1-UNC5C; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 70..2964
FT /tag= a
FT /product= "Human lROR-alpha-1-UNC5C protein"
XX
PN WO2004083371-A2.
XX
PD 30-SEP-2004.
XX
PF 16-MAR-2004; 2004WO-GB001124.
XX
PR 19-MAR-2003; 2003GB-00006185.
XX
PA (ASTR ) ASTRAZENECA AB.
PA (ASTR ) ASTRAZENECA UK LTD.
XX
PI Dahl N;
XX
XX WPI; 2004-691032/67.
XX P-PSDB; ADR99250.
XX
XX New isolated nucleic acid molecule encoding a RAR-like orphan receptor
XX alpha 1-uncordinated 5C (RORapproximate)l-UNC5C) polypeptide, useful
XX in diagnosing or treating obesity and hyperlipidemia.
XX
```

```
PS Claim 2; SEQ ID NO 1; 96pp; English.
XX
CC The invention relates to a novel isolated nucleic acid molecule, a
CC comprising a nucleotide sequence having at least 65% identity to a
CC degenerate variant of a fully defined sequence of 2986, 2780 or 1821 bp
CC (ADR99249, ADR99251 or ADR99255), or the complement of nucleotide
CC sequence with ADR99249, ADR99251 or ADR99255. The invention further
CC comprises an isolated nucleic acid molecule encoding a RAR-like orphan
CC receptor alpha 1-uncordinated 5C (ROR-alpha-1-UNC5C) polypeptide; an
CC isolated nucleic acid molecule encoding a ROR-alpha-5 polypeptide; a
CC vector comprising any of the nucleic acid molecules as cited; a host cell
CC comprising the vector; a purified fusion polypeptide of the ROR-alpha-1-
CC UNC5C polypeptide; a purified polypeptide of the ROR-alpha-5 polypeptide;
CC a method for producing a protein comprising culturing the host cell; a
CC method for detecting a polynucleotide which encodes a ROR-alpha-1-UNC5C
CC protein; a method for detecting the presence of an obesity susceptibility
CC gene; a method for detecting the presence of a translocation junction
CC between chromosome 4 at cytoband 4q 22.3 and chromosome 15 at cytoband
CC 15q22.2; a method for identifying a test compound that modulates the
CC expression of an obesity susceptibility gene identified in said method; a
CC method for identifying a test compound that modulates the activity of an
CC obesity protein encoded by the obesity susceptibility gene identified in
CC said method; a method for treating a subject having obesity; a
CC pharmaceutical composition comprising a compound identified in the
CC previous methods, and an adjuvant, diluent or carrier; making a
CC pharmaceutical composition; a method for determining if an obesity
CC susceptibility gene identified in the appropriate method; and a method
CC for diagnosing obesity, or a susceptibility to it in a subject. The
CC isolated nucleic acid molecules and compounds of the invention have the
CC following activities: anorectic, antilipaeamic, antiarteriosclerotic,
CC hepatotropic, hypotensive, antidiabetic, cardiant, vasotrophic,
CC osteopathic, antiarthritic, and cyostatic. The isolated nucleic acid
CC molecules and compounds may be used in gene therapy. The compound of an
CC modulating the activity of an obesity protein or the expression of an
CC obesity susceptibility gene is useful in the preparation of a medicament
CC for the treatment of obesity. The compound is also useful in treating or
CC diagnosing hyperlipidaemia, and the consequences of obesity, such as
CC arteriosclerosis, fatty liver, hypertension, diabetes, coronary heart
CC disease, stroke, gallbladder disease, osteoarthritis and cancer. This
CC polynucleotide sequence represents the gene encoding the human lROR-alpha
XX -1-UNC5C protein of the invention.
SQ Sequence 2986 BP; 770 A; 792 C; 770 G; 654 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.12e-16 Length: 2986
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 13 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x ADR99249 (1-2986)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 901 TCCACCTGGACGGAGTGTCTGTGTGTACAGCCGCTGTGGACGAGGTATCAGAAACGT 960
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 961 ACAAGGACTTGTACCAACCGGCACCACTCAATGGGGTGCCTTCTGTGAAGGCGCAGAGT 1020
Qy 41 ValGlnLysThrAlaCysAlaThrIleuCys 50
Db 1021 GTGCAGAAATAGCCTGTACTACGTTATGC 1050

RESULT 13
AA575738
ID AA575738 standard; cDNA; 3646 BP.
XX
AC AA575738;
XX
DT 13-FEB-2002 (first entry)
```

XX DNA encoding novel human diagnostic protein #11542.
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
OS
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX P-PSDB; ABG11551.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 1; SEQ ID NO 11542; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activities. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3646 BP; 930 A; 917 C; 921 G; 877 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 1,42e-16 Length: 3646
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 5 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AAS75738 (1-3646)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnIysArg 20
Db 944 TCCACCTGGACGGAGTGGTCTGTGTGTAAACAGCGCTGTGGACGAGGTATCAGAAACGT 1003
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 1004 ACAAGGACTTGTACCAACCCGACCACTCAATGGGGGTGCTCTGTGAAGGGCAGAGT 1063

Qy 41 ValGlnIysThrAlaCysAlaThrIleuCys 50
Db 1064 GTGCAGAAATAGCTGTACTACGTTATGC 1093
RESULT 14
ADR99257
ID ADR99257 standard; cDNA; 3646 BP.
XX AC ADR99257;
XX 16-DEC-2004 (first entry)
XX Human uncoordinated 5C (UNC5C) protein encoding cDNA.
XX
XX RAR-like orphan receptor alpha 1-uncoordinated 5C; ROR-alpha-1-UNC5C;
KW ROR-alpha-5; obesity; susceptibility; anorectic; antidiabetic;
KW antiarteriosclerotic; hepatotropic; hypotensive; antidiabetic; cardiant;
KW vasotropic; osteopathic; antiarthritic; cytostatic; gene therapy;
KW hyperlipidaemia; gene; human; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 155..2950
XX /*tag= a
XX /product= "Human uncoordinated 5C (UNC5C) protein"
XX
XX WO2004083371-A2.
XX
XX 30-SEP-2004.
XX
XX 16-MAR-2004; 2004WO-GB001124.
XX
XX 19-MAR-2003; 2003GB-00006185.
XX (ASTR) ASTRAZENECA AB.
XX (ASTR) ASTRAZENECA UK LTD.
XX
XX Dahl N;
XX
XX WPI; 2004-691032/67.
XX P-PSDB; ADR99258.
XX
XX New isolated nucleic acid molecule encoding a RAR-like orphan receptor
PT alpha 1-uncoordinated 5C (RORapproximate1-UNC5C) polypeptide, useful
PT in diagnosing or treating obesity and hyperlipidemia.
XX
XX Disclosure; SEQ ID NO 9; 96pp; English.
XX
XX The invention relates to a novel isolated nucleic acid molecule,
CC comprising a nucleotide sequence having at least 65% identity to a
CC degenerate variant of a fully defined sequence of 2986, 2780 or 1821 bp
CC (ADR99249, ADR99251 or ADR99255), or the complement of nucleotide
CC sequence with ADR99249, ADR99251 or ADR99255. The invention further
CC comprises: an isolated nucleic acid molecule encoding a RAR-like orphan
CC receptor alpha 1-uncoordinated 5C (ROR-alpha-1-UNC5C) polypeptide; an
CC isolated nucleic acid molecule encoding a ROR-alpha-5 polypeptide; a
CC vector comprising any of the nucleic acid molecules as cited; a host cell
CC comprising the vector; a purified fusion polypeptide of the ROR-alpha-1-
CC UNC5C polypeptide; a purified polypeptide of the ROR-alpha-5 polypeptide;
CC a method for producing a protein comprising culturing the host cell; a
CC method for detecting a polynucleotide which encodes a ROR-alpha-1-UNC5C
CC protein; a method for detecting the presence of an obesity susceptibility
CC gene; a method for detecting the presence of a translocation junction
CC between chromosome 4 at cytoband 4q 22.3 and chromosome 15 at cytoband
CC 15q22.2; a method for identifying a test compound that modulates the
CC expression of an obesity susceptibility gene identified in said method; a
CC method for identifying a test compound that modulates the activity of an
CC obesity protein encoded by the obesity susceptibility gene identified in
CC said method; a method for treating a subject having obesity; a
CC pharmaceutical composition comprising a compound identified in the
CC previous methods, and an adjuvant, diluent or carrier; making a
CC pharmaceutical composition; a method for determining if an obesity

PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX WPI; 2004-081935/08.
DR
DR P-PSDB; ADH71612.
XX
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 507; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator, and
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipase activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
XX encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 993 BP; 187 A; 306 C; 333 G; 167 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.33e-16	Length:	993
Score:	243.00	Matches:	42
Percent Similarity:	89.80%	Conservative:	2
Best Local Similarity:	85.71%	Mismatches:	5
Query Match:	83.79%	Indels:	0
DB:	12	Gaps:	0

US-10-624-932C-2_COPY_246_295 (1-50) x ADH71611 (1-993)

Qy	1	SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg	20
Db	661	TCGACGTGGACCGAGTGGTCCGTCTGCAGCCGACGCTGTGGCGGGCTGCGAGAACGG	720
Qy	21	SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn	40
Db	721	AGCGGAGCTGCACCAACCCGGCGCTCTCAACGGGGCGCTTTCTGTGAGGGGCAGAAAT	780
Qy	41	ValGlnLysThrAlaCysAlaThrIeu	49
Db	781	GTCCATGACCGACCGTCTCTCTCTG	807

Search completed: September 9, 2005, 00:42:51
Job time : 263.585 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:51:22 ; Search time 79.6984 Seconds
(without alignments)
1026.543 Million cell updates/sec

Title: US-10-624-932C-2_COPY_246_295

Perfect score: 290

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QWMT=fascap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US10624932 @cgn 1 1 187 @runat 08092005_161706_15822 -NCPU=6 -ICPU=3
-NO MWAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	290	100.0	3014	3	US-09-306-902A-1
3	249	85.9	3008	4	US-09-949-016-4794
4	249	85.9	114139	4	US-09-949-016-16536
5	238	82.1	2831	2	US-08-808-982-3
6	238	82.1	2831	3	US-09-306-902A-3
7	147	50.7	2820	4	US-09-854-845-15
8	147	50.7	2865	4	US-09-854-845-13
9	147	50.7	3105	4	US-09-854-845-5
10	147	50.7	3150	4	US-09-854-845-1
11	147	50.7	3237	4	US-09-854-845-7
12	147	50.7	3282	4	US-09-854-845-3

13	147	50.7	3411	4	US-09-854-845-11
14	147	50.7	3456	4	US-09-854-845-9
15	147	50.7	4074	4	US-09-854-845-17
16	139	47.9	3675	3	US-09-930-872-3
17	139	47.9	3675	4	US-10-217-774-3
18	139	47.9	3675	4	US-09-930-872-5
19	139	47.9	4042	3	US-09-930-872-5
20	136	46.9	457	4	US-09-270-767-31598
21	136	46.9	2006	4	US-09-270-767-15258
22	136	46.9	2114	3	US-09-130-491-7
23	132	45.5	4192	3	US-09-122-126B-1
24	132	45.5	4192	4	US-09-634-286A-1
25	132	45.5	4192	4	US-10-247-685-1
26	132	45.5	5722	4	US-09-657-472-1
27	131	45.2	3638	3	US-09-369-364A-8
28	130	44.8	2184	4	US-09-445-023A-2
29	130	44.8	2184	4	US-09-445-023A-13
30	130	44.8	3706	3	US-09-484-970B-58
31	130	44.8	3889	4	US-09-568-559-1
32	130	44.8	4676	3	US-09-130-491-1
33	130	44.8	4858	3	US-09-392-184-1
34	128.5	44.3	2853	4	US-10-009-332-2
35	128	44.1	7231	4	US-09-919-172-64
36	126	43.4	6659	4	US-09-321-987B-1
37	122	42.1	966	4	US-09-969-532-23
38	122	42.1	999	4	US-09-969-532-21
39	122	42.1	1008	4	US-09-969-532-19
40	122	42.1	1041	4	US-09-969-532-17
41	122	42.1	1659	4	US-09-969-532-7
42	122	42.1	1692	4	US-09-969-532-5
43	122	42.1	1701	4	US-09-969-532-3
44	122	42.1	1734	4	US-09-969-532-1
45	122	42.1	1968	4	US-09-969-532-31

ALIGNMENTS

RESULT 1

US-08-808-982-1
; Sequence 1, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-808-982-1
Alignment Scores:
Pred. No.: 2.36e-24 Length: 3014
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-624-932C-2_COPY_246_295 (1-50) x US-08-808-982-1 (1-3014)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGAGTGGTCCGCTCTGCAGCCCGAGCTGTGGCGGTGGCTGCAGAAACGG 795
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCCGGAGCTGCACCAACCGGCACCTCTCAACGGGGCGCTTCTGTGAGGGGCAGAAAT 855
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAAACAGCCTGCGCCACTCTGTGC 885
RESULT 2
US-09-306-902A-1
; Sequence 1, Application US/09306902A
; Patent No. 6271585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-306-902A-1
Alignment Scores:
Pred. No.: 2.36e-24 Length: 3014
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-624-932C-2_COPY_246_295 (1-50) x US-09-306-902A-1 (1-3014)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGAGTGGTCCGCTCTGCAGCCCGAGCTGTGGCGGTGGCTGCAGAAACGG 795
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCCGGAGCTGCACCAACCGGCACCTCTCAACGGGGCGCTTCTGTGAGGGGCAGAAAT 855
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAAACAGCCTGCGCCACTCTGTGC 885
RESULT 3
US-09-949-016-4794
; Sequence 4794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4794
; LENGTH: 3008
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-4794
Alignment Scores:
Pred. No.: 1.55e-19 Length: 3008
Score: 249.00 Matches: 41
Percent Similarity: 94.00% Conservative: 6
Best Local Similarity: 82.00% Mismatches: 3
Query Match: 85.86% Indels: 0
DB: 4 Gaps: 0
US-10-624-932C-2_COPY_246_295 (1-50) x US-09-949-016-4794 (1-3008)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 306 TCCACCTGGAGCGAGTGGTCTGTGTGTAAACAGCCGCTGTGGACGAGGTATCAGAAACGT 365
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 366 ACAAGGACTTGTACCAACCGGCACCACTCAATGGGGTGCCTTCTGTGAAGGCAGAGT 425
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 426 GTGCAGAAAATAGCTGTACTACTACGTATGTC 455
RESULT 4
US-09-949-016-16536
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-808-982-3

Alignment Scores:
Pred. No.: 2,82e-18 Length: 2831
Score: 238.00 Matches: 39
Percent Similarity: 86.00% Conservative: 4
Best Local Similarity: 78.00% Mismatches: 7
Query Match: 82.07% Indels: 0
DB: Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-08-808-982-3 (1-2831)

Qy 1 SerThrTrpThrCluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 742 TCCAGCTGGCGCAAAATGGTCACCCCTCTCTAAACCGCTGGCGCCGAGGTTGGCAGAAACGT 801
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 802 ACTAGGACCTGGCACCAACCCAGCCCACTCAATGGAGGTGCTTCTGGCAGGACAGGCT 861
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 862 TGCACAGAGAGCGCTTGCACCACCGTGTC 891

RESULT 6
US-09-306-902A-3
; Sequence 3, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627

```


; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3105
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-5

Alignment Scores:
Pred. No.: 1.57e-07 Length: 3105
Score: 147.00 Matches: 26
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 54.17% Mismatches: 16
Query Match: 50.69% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-854-845-5 (1-3105)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 2434 TCCTGCTGGACCTCATGGTCTCCATGCTCAGCTTCCTGTGGTGGGGTCACTATCAACGC 2493
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 2494 ACCCGTTCTGTGCACGAGCCCGCACCTCCCCAGGTGAGGACATCTGTCTCGGGCTGCAC 2553
Qy 41 ValGlnLysThrAlaCysAlaThr 48
Db 2554 ACGGAGGAGGCATATGTGCCACA 2577

RESULT 10
US-09-854-845-1
; Sequence 1, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3150
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-1

Alignment Scores:
Pred. No.: 1.6e-07 Length: 3150
Score: 147.00 Matches: 26
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 54.17% Mismatches: 16
Query Match: 50.69% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-854-845-1 (1-3150)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 2434 TCCTGCTGGACCTCATGGTCTCCATGCTCAGCTTCCTGTGGTGGGGTCACTATCAACGC 2493
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 2494 ACCCGTTCTGTGCACGAGCCCGCACCTCCCCAGGTGAGGACATCTGTCTCGGGCTGCAC 2553

Qy 41 ValGlnLysThrAlaCysAlaThr 48
Db 2554 ACGGAGGAGGCATATGTGCCACA 2577

RESULT 11

US-09-854-845-7
; Sequence 7, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3237
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-7

Alignment Scores:
Pred. No.: 1.66e-07 Length: 3237
Score: 147.00 Matches: 26
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 54.17% Mismatches: 16
Query Match: 50.69% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-854-845-7 (1-3237)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 2566 TCCTGCTGGACCTCATGGTCTCCATGCTCAGCTTCCTGTGGTGGGGTCACTATCAACGC 2625
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 2626 ACCCGTTCTGTGCACGAGCCCGCACCTCCCCAGGTGAGGACATCTGTCTCGGGCTGCAC 2685
Qy 41 ValGlnLysThrAlaCysAlaThr 48
Db 2686 ACGGAGGAGGCATATGTGCCACA 2709

RESULT 12

US-09-854-845-3
; Sequence 3, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3282

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; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-3

Alignment Scores:
Pred. No.: 1.69e-07 Length: 3282
Score: 147.00 Matches: 26
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 54.17% Mismatches: 16
Query Match: 50.69% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-854-845-3 (1-3282)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 2566 TCCTGCTGGACCTCATGTCTCCATGCTCAGCTTCCTGTGGGGGTCACTATCAACGC 2625
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 2626 ACCGGTTCCTGCACCGCCCGCACCTCCCGAGGTGAGGACATCTGTCTCGGGCTGCAC 2685
Qy 41 ValGlnLysThrAlaCysAlaThr 48
Db 2686 ACGGAGGAGGCATATGTGCCACA 2709

RESULT 13
US-09-854-845-11
; Sequence 11, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 3411
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-11

Alignment Scores:
Pred. No.: 1.78e-07 Length: 3411
Score: 147.00 Matches: 26
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 54.17% Mismatches: 16
Query Match: 50.69% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-854-845-11 (1-3411)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 2740 TCCTGCTGGACCTCATGTCTCCATGCTCAGCTTCCTGTGGGGGTCACTATCAACGC 2799
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 2800 ACCGGTTCCTGCACCGCCCGCACCTCCCGAGGTGAGGACATCTGTCTCGGGCTGCAC 2859
Qy 41 ValGlnLysThrAlaCysAlaThr 48
Db 2860 ACGGAGGAGGCATATGTGCCACA 2883
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RESULT 14
US-09-854-845-9
; Sequence 9, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 3456
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-9

Alignment Scores:
Pred. No.: 1.81e-07 Length: 3456
Score: 147.00 Matches: 26
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 54.17% Mismatches: 16
Query Match: 50.69% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-854-845-9 (1-3456)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 2740 TCCTGCTGGACCTCATGTCTCCATGCTCAGCTTCCTGTGGGGGTCACTATCAACGC 2799
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 2800 ACCGGTTCCTGCACCGCCCGCACCTCCCGAGGTGAGGACATCTGTCTCGGGCTGCAC 2859
Qy 41 ValGlnLysThrAlaCysAlaThr 48
Db 2860 ACGGAGGAGGCATATGTGCCACA 2883

RESULT 15
US-09-854-845-17
; Sequence 17, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4074
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-854-845-17

Alignment Scores:
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Pred. No.: 2.23e-07 Length: 4074
Score: 147.00 Matches: 26
Percent Similarity: 66.67% Conservative: 6
Best Local Similarity: 54.17% Mismatches: 16
Query Match: 50.69% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-854-845-17 (1-4074)

QY 1 SerThrTrrThrGluTrrSerValCysSerAlaSerCysGlyArgGlyTrrGlnLysArg 20
DB 2930 TCCTGCTGGACCTCATGGTCTCCATGCTCAGCTTCTGGTGGGGGTCACTATCAACGC 2989
QY 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
DB 2990 ACCCGTTCCTGCACCGCCCGCACCCCTCCCGAGGTGAGGACATCTGTCTCGGGCTGCAC 3049
QY 41 ValGlnLysThrAlaCysAlaThr 48
DB 3050 ACGAGGAGGACCTATGTGCCACA 3073

Search completed: September 9, 2005, 09:51:29
Job time : 94.6984 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: September 9, 2005, 04:41:16 ; Search time 498.956 Seconds
(without alignments)
658.098 Million cell updates/sec
Title: US-10-624-932C-2_COPY_246_295
Perfect score: 290
Sequence: 1 STWTWSVCSACRGWQK.....NGGAFCEQGNVQKTACATLC 50

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPECL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10624932 @CGN 1.1.989 @runat_08092005_161709_15882
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DBV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10J_NEW_PUB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	290	100.0	2697	16	US-10-240-154-15	Sequence 15, Appl
2	290	100.0	2752	10	US-09-918-779-1	Sequence 1, Appli
3	290	100.0	2752	18	US-10-624-932-1	Sequence 1, Appli
4	290	100.0	3014	10	US-09-933-261-1	Sequence 1, Appli
5	290	100.0	3014	14	US-10-256-702-1	Sequence 1, Appli
6	243	83.8	2881	10	US-09-970-944-1	Sequence 31, Appl
7	239	82.4	168	21	US-10-872-681-31	Sequence 117, App
8	239	82.4	2181	17	US-10-094-886-117	Sequence 53, Appl
9	239	82.4	2661	21	US-10-872-681-53	Sequence 1, Appli
10	239	82.4	2860	17	US-10-087-684-1	Sequence 3, Appli
11	239	82.4	2860	17	US-10-087-684-3	Sequence 1, Appli
12	239	82.4	2860	17	US-10-218-779-1	Sequence 3, Appli
13	239	82.4	2860	17	US-10-218-779-3	Sequence 55, Appl
14	239	82.4	2868	21	US-10-872-681-55	Sequence 37, Appl
15	239	82.4	2895	18	US-10-037-417-37	Sequence 115, App
16	239	82.4	2898	17	US-10-094-886-115	Sequence 136, App
17	239	82.4	2979	19	US-10-473-518-136	Sequence 55, Appl
18	239	82.4	2995	11	US-09-972-211-55	Sequence 55, Appl
19	239	82.4	2995	18	US-10-096-625-55	Sequence 18, Appl
20	239	82.4	3485	9	US-09-816-828-18	Sequence 1123, Ap
21	239	82.4	3501	17	US-10-295-027-1123	Sequence 145, App
22	239	82.4	3884	14	US-10-028-072-145	Sequence 145, App
23	239	82.4	3884	14	US-10-140-808-145	Sequence 145, App
24	239	82.4	3884	14	US-10-121-049-145	Sequence 145, App
25	239	82.4	3884	14	US-10-123-904-145	Sequence 145, App
26	239	82.4	3884	14	US-10-140-470-145	Sequence 145, App
27	239	82.4	3884	14	US-10-175-746-145	Sequence 145, App
28	239	82.4	3884	14	US-10-176-918-145	Sequence 145, App
29	239	82.4	3884	14	US-10-176-921-145	Sequence 145, App
30	239	82.4	3884	14	US-10-137-865-145	Sequence 145, App
31	239	82.4	3884	14	US-10-140-474-145	Sequence 145, App
32	239	82.4	3884	14	US-10-142-431-145	Sequence 145, App
33	239	82.4	3884	14	US-10-143-114-145	Sequence 145, App
34	239	82.4	3884	14	US-10-142-419-145	Sequence 145, App
35	239	82.4	3884	14	US-10-123-262-145	Sequence 145, App
36	239	82.4	3884	14	US-10-142-423-145	Sequence 145, App
37	239	82.4	3884	14	US-10-121-050-145	Sequence 145, App
38	239	82.4	3884	14	US-10-141-755-145	Sequence 145, App
39	239	82.4	3884	14	US-10-143-032-145	Sequence 145, App
40	239	82.4	3884	14	US-10-123-108-145	Sequence 145, App
41	239	82.4	3884	14	US-10-123-236-145	Sequence 145, App
42	239	82.4	3884	14	US-10-123-261-145	Sequence 145, App
43	239	82.4	3884	14	US-10-140-921-145	Sequence 145, App
44	239	82.4	3884	14	US-10-140-928-145	Sequence 145, App
45	239	82.4	3884	14	US-10-121-045-145	Sequence 145, App

ALIGNMENTS

RESULT 1
US-10-240-154-15
; Sequence 15, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CKFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240.154
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 2697

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; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15
Alignment Scores:
Pred. No.: 6.16e-27 Length: 2697
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0
US-10-624-932c-2_COPY_246_295 (1-50) x US-10-240-154-15 (1-2697)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 736 TCGACGTGGAGTGGTGGTCCGCTGCGAGCCCGAGCTGTGGCGCTGGCAGAAACGG 795
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 796 AGCCGGAGCTGCACCAACCCGACCTCTCAACGGGGCGGCTTCTGTGAGGGGCAGAAAT 855
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 856 GTCCAGAAAACAGCCTGCGCCACTCTGTGC 885
RESULT 2
US-09-918-779-1
; Sequence 1, Application US/09918779
; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Leplev, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
;
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15
Alignment Scores:
Pred. No.: 6.16e-27 Length: 2697
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0
US-10-624-932c-2_COPY_246_295 (1-50) x US-09-918-779-1 (1-2752)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 781 TCGACGTGGAGTGGTGGTCCGCTGCGAGCCCGAGCTGTGGCGCTGGCAGAAACGG 840
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 841 AGCCGGAGCTGCACCAACCCGACCTCTCAACGGGGCGGCTTCTGTGAGGGGCAGAAAT 900
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 901 GTCCAGAAAACAGCCTGCGCCACTCTGTGC 930
RESULT 3
US-10-624-932-1
; Sequence 1, Application US/10624932
; Publication No. US20040096877A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Leplev, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/10/624,932
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918,779
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
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/ APPLICATION NUMBER: 08/808,982
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: OSMAN, RICHARD A
/ REGISTRATION NUMBER: 36,627
/ REFERENCE/DOCKET NUMBER: UC96-217
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 343-4341
/ TELEFAX: (415) 343-4342
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3014 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-933-261-1

Alignment Scores:
Pred. No.: 6,96e-27 Length: 3014
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-09-933-261-1 (1-3014)

QY 1 SerThrTpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
DB 736 TCGAGCTGGACTGAGTGGTCCGTCTGCAGGCCACGCTGTGGGGTGGCTGGCAGAACCG 795
QY 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
DB 796 AGCCGGAGCTGCACCAACCCGGGCACCTCTCAACGGGGGCCCTTCTGTGTGAGGGGCGAAT 855
QY 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
DB 856 GTCCAGAAACAGCCTGCGCCACTCTGTGC 885

RESULT 5
US-10-256-702-1
/ Sequence 1, Application US/10256702
/ Publication No. US20030059859A1
/ GENERAL INFORMATION:
/ APPLICANT: Tessier-Lavigne, Marc
/ Leonardo, E. David
/ Hink, Lindsey
/ Masu, Masayuki
/ Kazuko, Keino-Masu
/ TITLE OF INVENTION: Netrin Receptors
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
/ STREET: 268 BUSH STREET, SUITE 3200
/ CITY: SAN FRANCISCO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/256,702
/ FILING DATE: 27-Sep-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/933,261
/ FILING DATE: 20-Aug-2001
/ APPLICATION NUMBER: 08/808,982

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Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 322 TCGACGTGGACCGAGTGTCCGTCTGCAGCGCCAGCTGTGGGCGCGCTGGCAGAAACGG 891
Qy 21 SerArgSerCysThrAsnProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 882 AGCCGGAGCTGCACCAACCCGGCGCTCTCAACGGGGGCGCTTCTGTGAGGGGACAGAT 941
Qy 41 ValGlnLysThrAlaCysAlaThrLeu 49
Db 942 GTCCATGACCGACCGCTCTCTCTCTG 968

RESULT 7
US-10-872-681-31
; Sequence 31, Application US/10872681
; Publication No. US20050026251A1
; GENERAL INFORMATION:
; APPLICANT: ARES TRADING LIMITED
; TITLE OF INVENTION: TRANSMEMBRANE PROTEIN
; FILE REFERENCE: P029209WO
; CURRENT APPLICATION NUMBER: US/10/872,681
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: GB0130721.4
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 31
; LENGTH: 168
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SEQ ID NO:9
US-10-872-681-31

Alignment Scores:
Pred. No.: 9.93e-22 Length: 168
Score: 239.00 Matches: 38
Percent Similarity: 86.00% Conservative: 5
Best Local Similarity: 76.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 21 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-872-681-31 (1-168)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 15 TCTTCTGGACAGAGTGTGCAGCTGCAATGTTCCGTGTGTGTAGAGATGGCAGAAACGT 74
Qy 21 SerArgSerCysThrAsnProAlaProLeuAenGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 75 TCCCGAGCTCTGCACCAACCCAGCTCTCTCAATGTTGGGCGCTTTTGTGAGGGAATGTCA 134
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 135 GTGCAGAAATAAACCCTGCACCTCTCTTGT 164

RESULT 8
US-10-094-886-117
; Sequence 117, Application US/10094886
; Publication No. US20040002120A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Vernet, Corine A.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc
; APPLICANT: Guo, Xiaojia

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Db 986 GTGCAGAAAATAACCTGCACTTCCTTTGT 1015
||||||| ||| :::|||||

RESULT 9
US-10-872-681-53
; Sequence 53, Application US/10872681
; Publication No. US20050026251A1
; GENERAL INFORMATION:
; APPLICANT: ARES TRADING LIMITED
; TITLE OF INVENTION: TRANSMEMBRANE PROTEIN
; FILE REFERENCE: P029209WO
; CURRENT APPLICATION NUMBER: US/10/872,681
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: GB0130721.4
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 53
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SEQ ID NO:31
US-10-872-681-53

Alignment Scores:
Pred. No.: 2,09e-20 Length: 2661
Score: 239.00 Matches: 38
Percent Similarity: 86.00% Conservative: 5
Best Local Similarity: 76.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 21 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-872-681-53 (1-2661)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnIlysArg 20
|||::|||:|||||
Db 643 TCTTCTCGGACAGAGTGCTGACGCTGCAATGTCCTGCTGTGGTAGAGGATGGCAGAAACGT 702
|||::|||:|||||

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAen 40
|||::|||:|||||

Db 703 TCCCGGACCTGCACCACCCAGCTCCTCTCAATGTTGGGGGCTTTTGTGAGGAATGTCA 762
|||::|||:|||||

Qy 41 ValGlnIysThrAlaCysAlaThrLeuCys 50
|||::|||:|||||

Db 763 GTGCAGAAAATAACCTGCACTTCCTTTGT 792
||||||| ||| :::|||||

RESULT 10
US-10-087-684-1
; Sequence 1, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muraldhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchertnev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malvankar, Uriel M.

```
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 1
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-1

Alignment Scores:
Pred. No.: 2,26e-20 Length: 2860
Score: 239.00 Matches: 39
Percent Similarity: 86.00% Conservative: 4
Best Local Similarity: 78.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 17 Gaps: 0

US-10-624-932c-2_COPY_246_295 (1-50) x US-10-087-684-1 (1-2860)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 806 TCCAGCTGGGCAGAGTGTGTCCACCGCTGTGCGCCGAGGCTGGCAGAGGCGC 865

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 866 ACCCGACCTGCACCAACCCCGCTCCACTCAACGAGGGGGCTTTCTGCGAGGGCCAGGCA 925

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 926 TTCAGAGAGACCGCTGCACCACCATCTGC 955

RESULT 11
US-10-087-684-3
; Sequence 3, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
```

```
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 3
; LENGTH: 2860
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(2857)
US-10-087-684-3

Alignment Scores:
Pred. No.: 2,26e-20 Length: 2860
Score: 239.00 Matches: 39
Percent Similarity: 86.00% Conservative: 4
Best Local Similarity: 78.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 17 Gaps: 0

US-10-624-932c-2_COPY_246_295 (1-50) x US-10-087-684-3 (1-2860)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 806 TCCAGCTGGGCAGAGTGTGTCCACCGCTGTGCGCCGAGGCTGGCAGAGGCGC 865

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 866 ACCCGACCTGCACCAACCCCGCTCCACTCAACGAGGGGGCTTTCTGCGAGGGCCAGGCA 925

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 926 TTCAGAGAGACCGCTGCACCACCATCTGC 955

RESULT 12
US-10-218-779-1
; Sequence 1, Application US/10218779
; Publication No. US20040029222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel
; APPLICANT: Burgess, Catherine
```

APPLICANT: Casman, Stacie
APPLICANT: Spytek, Kimberly
APPLICANT: Boldog, Ferenc
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Mishra, Vishnu
APPLICANT: Patturajan, Meera
APPLICANT: Shenoy, Suresh
APPLICANT: Rastelli, Luca
APPLICANT: Tchernev, Velizar
APPLICANT: Vernet, Corine
APPLICANT: Zerhusen, Bryan
APPLICANT: Malyankar, Uriel
APPLICANT: Guo, Xiaojia
APPLICANT: Miller, Charles
APPLICANT: Gangolli, Esha
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-214
CURRENT APPLICATION NUMBER: US/10/218,779
CURRENT FILING DATE: 2002-08-14
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 60/253,834
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/250,926
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/264,180
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/313,656
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/327,456
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2860
TYPE: DNA
ORGANISM: Homo sapiens
US-10-218-779-1

Alignment Scores:
Pred. No.: 2,26e-20 Length: 2860
Score: 239.00 Matches: 39
Percent Similarity: 86.00% Conservative: 4
Best Local Similarity: 78.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 17 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-218-779-1 (1-2860)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 806 TCCAGCTGGGCAGAGTGGTCCACCTGCTCCAAACCGCTGTGGCCGAGGCTGGCAGAAAGCGC 865

Qy 21 SerArgSerCysThrAsnProAlaProLeuHengGlyAlaPheCysGluGlyGlnAsn 40
Db 866 ACCCGGACCTGCACCAACCCGCTCCACTCAACGAGGGGCTTCTTGGAGGGCCAGGCA 925

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 926 TTCCAGAAGACCGCTGCACCATCTGCG 955

RESULT 13
US-10-218-779-3
Sequence 3, Application US/10218779
Publication No. US2004002922A1
GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit
APPLICANT: MacDougall, John
APPLICANT: Millet, Isabelle
APPLICANT: Ellerman, Karen
APPLICANT: Stone, David
APPLICANT: Gerlach, Valerie
APPLICANT: Grosse, William
APPLICANT: Alsbrook II, John

APPLICANT: Lepley, Denise
APPLICANT: Rieger, Daniel
APPLICANT: Burgess, Catherine
APPLICANT: Casman, Stacie
APPLICANT: Spytek, Kimberly
APPLICANT: Boldog, Ferenc
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Mishra, Vishnu
APPLICANT: Patturajan, Meera
APPLICANT: Shenoy, Suresh
APPLICANT: Rastelli, Luca
APPLICANT: Tchernev, Velizar
APPLICANT: Vernet, Corine
APPLICANT: Zerhusen, Bryan
APPLICANT: Malyankar, Uriel
APPLICANT: Guo, Xiaojia
APPLICANT: Miller, Charles
APPLICANT: Gangolli, Esha
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-214
CURRENT APPLICATION NUMBER: US/10/218,779
CURRENT FILING DATE: 2002-08-14
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 60/253,834
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/250,926
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/264,180
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/313,656
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/327,456
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 2860
TYPE: DNA
ORGANISM: Homo sapiens
US-10-218-779-3

Alignment Scores:
Pred. No.: 2,26e-20 Length: 2860
Score: 239.00 Matches: 39
Percent Similarity: 86.00% Conservative: 4
Best Local Similarity: 78.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 17 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-218-779-3 (1-2860)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 806 TCCAGCTGGGCAGAGTGGTCCACCTGCTCCAAACCGCTGTGGCCGAGGCTGGCAGAAAGCGC 865

Qy 21 SerArgSerCysThrAsnProAlaProLeuHengGlyAlaPheCysGluGlyGlnAsn 40
Db 866 ACCCGGACCTGCACCAACCCGCTCCACTCAACGAGGGGCTTCTTGGAGGGCCAGGCA 925

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 926 TTCCAGAAGACCGCTGCACCATCTGCG 955

RESULT 14
US-10-872-681-55
Sequence 55, Application US/10872681
Publication No. US2005002625A1
GENERAL INFORMATION:
APPLICANT: ARES TRADING LIMITED
TITLE OF INVENTION: TRANSMEMBRANE PROTEIN
FILE REFERENCE: P029209WO
CURRENT APPLICATION NUMBER: US/10/872,681
CURRENT FILING DATE: 2004-06-21

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; PRIOR APPLICATION NUMBER: GB0130721.4
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 55
; LENGTH: 2868
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SEQ ID NO:33
US-10-872-681-55

Alignment Scores:
Pred. No.: 2.27e-20 Length: 2868
Score: 239.00 Matches: 38
Percent Similarity: 86.00% Conservative: 5
Best Local Similarity: 76.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 21 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-872-681-55 (1-2868)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 808 TCCTCTGGACAGAGTGGTCAGCCTGCAATGTCGCTGTGTAGAGGATGGCAGAAACGT 867

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 868 TCCCGGACCTGCACCAACCCAGCTCCTCAATGTTGGGGCCCTTTGTGAGGGAATGTCA 927

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 928 GTGCAGAAATAAATACCTGCACCTCTCTTTGT 957

RESULT 15
US-10-037-417-37
; Sequence 37, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 2895
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-037-417-37

Alignment Scores:
Pred. No.: 2.3e-20 Length: 2895
Score: 239.00 Matches: 39
Percent Similarity: 86.00% Conservative: 4
Best Local Similarity: 78.00% Mismatches: 7
Query Match: 82.41% Indels: 0
DB: 18 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x US-10-037-417-37 (1-2895)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 778 TCCAGCTGGGCGAGAGTGGTCACCTGTCTCAACCGCTGTGGCCGAGGCTGGCAGAGCGC 837

Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyGlyAlaPheCysGluGlyGlnAsn 40
Db 838 ACCCGACCTGCACCAACCCGCTCCCACTCAACGAGGGGCGCTTCTGGAGGGGCCAGGCA 897

Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 898 TTCCAGAGAGCCGCTGCACCACTATCTGC 927

Search completed: September 9, 2005, 18:52:17
Job time : 502.956 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 22:38:37 ; Search time 1645.59 Seconds
(without alignments)
1156.553 Million cell updates/sec

Title: US-10-624-932c-2_copy_246_295

Perfect score: 290

Sequence: 1 STWTSMVSCSACRGWQK.....NGGAFCEGQNVQKTACATLC 50

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10624932/runat_08092005_161706_15792/app_query.fasta_1.1386
-DB=EST -QFMT=fastap -SURFIX=first -MINMATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=spct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CNC 1 1 8180 @runat_08092005_161706_15792 -NCPU=6 -ICPU=3
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_g881.*
9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290	100.0	500	8	BZ921959
2	287	99.0	548	5	BX452510
3	253	87.2	967	5	BU468894
4	249	85.9	351	5	BY020742
5	249	85.9	602	9	CR012607
6	249	85.9	856	7	CN164143
7	249	85.9	875	7	CO807001
8	249	85.9	2791	9	AY406493
9	249	85.9	2802	9	AY406491

10	249	85.9	2802	9	AY406492
11	249	85.9	3790	3	AK031655
12	240	82.8	774	5	BU365958
13	239	82.4	594	6	CA771550
14	239	82.4	681	2	BF313643
15	239	82.4	733	5	BX200046
16	239	82.4	812	5	BX915627
17	239	82.4	2507	9	AY401470
18	239	82.4	2532	9	AY411747
19	239	82.4	2775	9	AY401469
20	238	82.1	386	6	CB806444
21	238	82.1	679	2	BF098738
22	238	82.1	679	7	CO045001
23	238	82.1	693	6	CB246544
24	238	82.1	801	7	CV110922
25	238	82.1	2532	9	AY411749
26	238	82.1	2775	9	AY401471
27	238	82.1	3866	3	AK018177
28	236	81.4	720	1	A1959236
29	235	81.0	577	7	CO670344
30	229	79.0	354	4	BM257107
31	228	78.6	487	5	BQ037844
32	228	78.6	709	1	AJ729963
33	228	78.6	746	5	BX872585
34	228	78.6	751	5	BX871388
35	228	78.6	1175	5	CL642218
36	225	77.6	632	2	BE314077
37	223	76.9	459	2	BE700724
38	219	75.5	459	2	BE700724
39	217	74.8	801	8	BZ880721
40	214	73.8	969	2	BF206813
41	213	73.4	605	5	BX913103
42	210	72.4	1054	9	CNS02H8B
43	170.5	58.8	2532	9	AY411748
44	165	56.9	453	7	CN626234
45	164	56.6	1034	4	BI758231

ALIGNMENTS

RESULT 1

BZ921959/c

LOCUS

DEFINITION

BZ921959 500 bp DNA linear GSS 12-JUN-2003

CH240_120K19.TJ CHORI-240 Bos taurus genomic clone CH240_120K19,

genomic survey sequence.

ACCESSION BZ921959

VERSION BZ921959.1

KEYWORDS GI:31647345

SOURCE GSS.

ORGANISM Bos taurus (cow)

Bos taurus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovinae; Bos.

1 (bases 1 to 500)

Larkin,D.M., Everts-van der Wind,A., Rebeiz,M., Schweitzer,P.,

Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L.,

Womack,J.E., de Jong,P.J. and Lewin,H.A.

A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human

Genome Sequence

Unpublished (2003)

Contact: Harris Lewin

Department of Animal Sciences

University of Illinois at Urbana Champaign

1201 W. Gregory Dr., Urbana, IL 61801, USA

Tel: 217 333 5998

Fax: 217 244 5617

Email: h.lewin@uiuc.edu

Clones are derived from the bovine BAC library CHORI-240

(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.choi.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/ordering_information.html). This work

was undertaken as part of the International Bovine BAC Mapping

AY406492	Pan trogl
AK031655	Mus muscu
BU365958	603785840
CA771550	io72f10.Y
BF313643	601900292
BX200046	BX200046
BX915627	BX915627
AY401470	Pan trogl
AY411747	Homo sapi
AY401469	Homo sapi
CB806444	AMGNNUC.N
BF098738	601750874
CO045001	UI-M-G10-
CB246544	UI-M-F10-
CV110922	AGENCOURT
AY411749	Mus muscu
AY401471	Mus muscu
AK018177	Mus muscu
A1959236	fd25g10.Y
CO670344	DG33-5803
BM257107	520613 MA
BQ037844	pgn1c.p40
AJ729963	AJ729963
BX872585	BX872585
BX871388	BX871388
CL642218	CH213-26B
BE314077	601146259
BE700724	QV1-NN010
BZ880721	CH240_233
BF206813	601870209
BX913103	BX913103
AL97300	Tetraodon
AY411748	Pan trogl
CN626234	tae56d02
BI758231	603029876

Consortium (IBBMC) by the University of Illinois at Urbana
Champaign, USA with funds provided by grant No. AG202-34480-11828
from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock
Genome Sequencing Initiative)
Plate: 120 row: K column: 19
Seq primer: SP6
Class: BAC ends.

FEATURES

Location/Qualifiers
1..500
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_120K19"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Alignment Scores:
Pred. No.: 1.2e-20 Length: 500
Score: 290.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x BZ921959 (1-500)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 418 TCGAGCTGGACTAGTGGTCTCTGTCAGCGCCAGCTGTGGCGCGGCTGGCAGAAAAGG 359
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyGlnAsn 40
Db 358 AGCCGGAGCTGCACCAACCCGCGCTCTCAACGGGGGTGCTTCTGTGAGGGGCGAGAT 299
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 298 GTCCAGAAAACAGCTGCGCCACCCTGTGTC 269

RESULT 2
BX452510
LOCUS
DEFINITION BX452510 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
CS0DN001YE16 5-PRIME, mRNA sequence.
ACCESSION BX452510
VERSION BX452510.2 GI:47063451
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 548)
Li.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31026396.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3529.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS0BAG0692F06_CS06574_lkc=3529.f

FEATURES

Location/Qualifiers
1..548
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN001YE16"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 2.76e-20 Length: 548
Score: 287.00 Matches: 49
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.00% Mismatches: 0
Query Match: 98.97% Indels: 0
DB: 5 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x BX452510 (1-548)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 230 TCGACGTGGACCGAGTGGTCCGCTGTCAGCGCCAGCTGTGGCGCGGTTGGCAGAAACGG 289
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyGlnAsn 40
Db 290 AGCCGGAGCTGCACCAACCCGCGCTCTCAACGGGGGTGCTTCTGTGAGGGGCGAGAT 349
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 350 GTTCAGAAAACAGCTGCGCCACCCTGTGTC 379

RESULT 3
BU468894
LOCUS
DEFINITION BU468894 603363436F1 CSEQBN21 Gallus gallus cDNA clone CHEST258h9 5', mRNA
sequence.
ACCESSION BU468894
VERSION BU468894.1 GI:25962471
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 967)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
PUBLISHED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

Location/Qualifiers
1..967
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"


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Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyGlnAsn 40
Db 247 ACAAGAACCTGCACCAATCCAGCTCCACTCAATGCGGGGCTTCTGTGTGAGGGCAGAGT 306
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 307 GTGCAGAAAATAGCATGCACCTACGTTATGT 336

RESULT 5
LOCUS CR012607 602 bp DNA linear GSS 05-JUL-2004
DEFINITION Reverse strand read from insert in 5'HPRT insertion targeting and
chromosome engineering clone MHPN277n18, genomic survey sequence.
ACCESSION CR012607.1 GI:49745653
VERSION 94.00%
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 602)
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J. and Bradley,A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICR
FEATURES
source
1..602
location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone_lib="MHPN277n18"
/clone_libs="MHPN"

ORIGIN
Alignment Scores: 3.11e-16 Length: 602
Pred. No.: 249.00 Matches: 41
Score: 94.00% Conservative: 6
Percent Similarity: 82.00% Mismatches: 3
Best Local Similarity: 85.86% Indels: 0
Query Match: 9 Gaps: 0
DB:

US-10-624-932C-2_COPY_246_295 (1-50) x CR012607 (1-602)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 451 TCCACCTGGACAGAGTGGTCTGTGTAAACAGCCGCTGTGGCGGAGGATATCAGAAACGC 510
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyGlnAsn 40
Db 511 ACAAGAACCTGCACCAACCCAGCCCACTCAATGTTGGGGCTTCTGTGTGAGGGCAGAGT 570
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 571 GTGCAGAAAATAGCATGCACCTACGTTATGT 600

RESULT 6
LOCUS CN164143 856 bp mRNA linear EST 02-APR-2004
DEFINITION 994266 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION CN164143
VERSION CN164143.1 GI:46178573
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 856)
AUTHORS Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Nonneman,D.J., Wray,J.E. and Keele,J.W.

TITLE Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: TW8062 row: N column: 14
Seq primer: GTAATACGACTCACTATAGG.
FEATURES
source
1..856
location/Qualifiers
/organism="Sus scrofa"
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/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4P1G"
/note="vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

ORIGIN
Alignment Scores: 4.7e-16 Length: 856
Pred. No.: 249.00 Matches: 41
Score: 94.00% Conservative: 6
Percent Similarity: 82.00% Mismatches: 3
Best Local Similarity: 85.86% Indels: 0
Query Match: 7 Gaps: 0
DB:

US-10-624-932C-2_COPY_246_295 (1-50) x CN164143 (1-856)
Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
Db 566 TCCACCTGGACAGAGTGGTCTGTGTAAACAGCCGCTGTGGCGGAGGATATCAGAAACGC 625
Qy 21 SerArgSerCysThrAsnProAlaProLeuAsnGlyAlaPheCysGluGlyGlnAsn 40
Db 626 ACAAGAACCTGCACCAATCCAGCCCACTCAATGTTGGCTTCTGTGTGAGGGCAGAGT 685
Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 686 GTGCAGAAAATAGCATGCACCTACGTTATGT 715

RESULT 7
LOCUS CO807001 875 bp mRNA linear EST 06-AUG-2004
DEFINITION AGENCOURT 30255333 NIH MGC 257 Mus musculus cDNA clone
IMAGE:30932367 5', mRNA sequence.
ACCESSION CO807001
VERSION CO807001.1 GI:51022265
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 875)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: csapbs-r@mail.nih.gov
Tissue Procurement: Dr. Kathleen Horner, Stanford University
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

```

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM1181 row: i column: 16
 High quality sequence stop: 671.

Location/Qualifiers
 1..875

FEATURES

source
 1..875
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:3092367"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_257"
 /note="Organ: occyte; Vector: pExpress-1; Site 1: EcoRV;
 Site 2: NotI; cDNA was primed using oligo-dT primer:
 5'-pGACTAGTCTAGATCGGAGCGGCC(T)25-3' and cloned into
 the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb
 resulted in an average insert size of 1.0kb. This is a
 normalized library (primary library is NIH_MGC_256) and
 was constructed by Express Genomics (Frederick, MD). Note:
 this is a NIH_MGC library"

ORIGIN

Alignment Scores:
 Pred. No.: 4,828-16 Length: 875
 Score: 249.00 Matches: 41
 Percent Similarity: 94.00% Conservative: 6
 Best Local Similarity: 82.00% Mismatches: 3
 Query Match: 85.86% Indels: 0
 DB: 7 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x C0807001 (1-875)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
 Db 181 TCCACCTGACAGAGTGGTCTGTGTAAACCCCGCTGTGGCGGAGGATATCAGAAACGC 240
 Qy 21 SerArgSerCysThrAsnProAlaProLeuAangGlyGlyAlaPheCysGluGlyGlnAsn 40
 Db 241 ACAAGAACCTGCACCAACCCACCCCACTCAATGTGGGGCTTCTGTGAGGGGCGAGAGT 300
 Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
 Db 301 GTGCAGAAATAGCATGCACCTACGTTATGT 330

RESULT 8
 AY406493
 LOCUS
 DEFINITION
 Mus musculus UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION
 AY406493
 VERSION
 AY406493.1 GI:39762467
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 2791)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios
 Science 302 (5652), 1960-1963 (2003)
 14671302

2 (bases 1 to 2791)

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission

TITLE

JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES

source
 1..2791
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 <1..>2791
 /gene="UNC5C"
 /locus_tag="HMC2575"

ORIGIN

Alignment Scores:
 Pred. No.: 1,888-15 Length: 2791
 Score: 249.00 Matches: 41
 Percent Similarity: 94.00% Conservative: 6
 Best Local Similarity: 82.00% Mismatches: 3
 Query Match: 85.86% Indels: 0
 DB: 9 Gaps: 0

US-10-624-932C-2_COPY_246_295 (1-50) x AY406493 (1-2791)

Qy 1 SerThrTrpThrGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnLysArg 20
 Db 785 TCCACCTGACAGAGTGGTCTGTGTAAACCCCGCTGTGGCGGAGGATATCAGAAACGC 844
 Qy 21 SerArgSerCysThrAsnProAlaProLeuAangGlyGlyAlaPheCysGluGlyGlnAsn 40
 Db 845 ACAAGAACCTGCACCAACCCACCCCACTCAATGTGGGGCTTCTGTGAGGGGCGAGAGT 904
 Qy 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
 Db 905 GTGCAGAAATAGCATGCACCTACGTTATGT 934

RESULT 9

LOCUS

AY406491
 Homo sapiens UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.

ACCESSION
 AY406491

VERSION
 AY406491.1 GI:39762465

KEYWORDS
 GSS.

SOURCE
 Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 2802)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission

Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

REFERENCE

AUTHORS

2 (bases 1 to 2802)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission

TITLE

JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES

source
 1..2802
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 <1..>2802

gene

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohseato, N., Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sugabe, Y., Tegami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

RNA library was prepared and sequenced in mouse genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>.

FEATURES

```

1.3790
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:6030473H24"
/db_xref="taxon:10090"
/clone="6030473H24"
/sex="male"
/tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"

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CDS

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/Note="unnamed protein product; putative
unb homolog (C. elegans) 3 (MGD|GI:1095412,
GB|NM_009472, evidence: BLASTN, 99%, match=464)"
/codon_start=1
/protein_id="BAC27495.1"
/db_xref="GI:26327503"
/translation="MRKGLRATARCGLIGYQLQMLPALALLSASGTGSAQDDDE
FFHELPEYFPSPDPELPHLEIPEEAYIVKKNPVNLYKCAKPATQYFKCNSEWVHQ
KHVVDEAVDETSGLIVREVSIEISRQVEELPGPEYWCQCVAWSAGSTKSRKAYV
IADURKTEQELGVEEGSEGLVEGLVQVQVQVQVQVQVQVQVQVQVQVQVQVQV
TDHNLNLIKQARLSDTANTYCAKNIIVAKRQKSTATTIVYVNGWSTWSTWSTWSTW
GRGYQKRTCTNPAPLNGGATCGVQKQKIACTTLCVDPDQVSTWSTWSTWSTWSTW
WRRECTAPAPNGKDCDGLVLQKNCSTDCQMGQFIPYISTEHRPQNGYGFSSADP
SDDAVALYQIVLAVTVCGLTIVVVALFVYKKNHRDFESDIIDSALNQGFGPVNIAA
RQDLALPEPLTSPAAQYGGPVVLAHDVSDKIPTMNSPLDPLPNLKIYVNSSGAVT
QODLLAEPSKLSPOMTQSLINEALNKQSLAROTDPSCTAGTNSLGGHLIIPN
SGVSLLIIPAGIIPQGVRYEMVTVHKKENRPMPEBSQILLTVPVSCGPPGALLTRPV
LTLHPCADSTTKAAKRLUKLAIFGLPQCDSSVVVYBGENFTPTCIQIDBAACHILTE
LSTVALVGOSTTAAKRLUKLAIFGLPQCDSSVVVYBGENFTPTCIQIDBAACHILTE
GQLLEPKALRFKGSIHNLRLSHIDIAHLSMKLLAKYQEIFPHYHWSGQRNLTK
TFTLEERLSNLVELVCKLQVROVEGSGQIFQLNCTVSEEPGTGIDPLLPDASTITVTY
GPSAFSIPILPIRQKLCSSLDAPTRGHDNRMLAKHLNRLYLVNFVATKSPSTGTGVL
DDNPPDGNISMLAAVLPEMGRHETVTVYLAARGSV"

```

ORIGIN

Alignment Scores:	
Pred. No.:	2.7e-15
Score:	249.00
Percent Similarity:	94.00%
Best Local Similarity:	82.00%
Query Match:	85.86%
DB:	3
Length:	3790
Matches:	41
Conservative:	6
Mismatches:	3
Indels:	0
Gaps:	0

US-10-624-932C-2 COPY 246 295 (1-50) x AK031655 (1-3790)

QY
1 SerThrTrpGluTrpSerValCysSerAlaSerCysGlyArgGlyTrpGlnIysArg 20

Db		907	TCCACCTGGACAGAGTGGTGTTGTTGAACAGCCCGCTGTGGCGAGATATCAGAACC	GCG	966
Qy	21	SerArgSerCysThrAnProAlaProLeuAenGlyGlyAlaPheCysGluGI ₁ GlnAsn	40		
Db		967	AAAGAACCTTCGCACCAACCCAGCCCCCACCAATGGTGGGGGCCCTTCTGTGAGGGGCAGAGT	1026	
Qy	41	ValGlnLysThrAlaCysAlaThrLeuCys	50		
Db		1027	GTGCAGAAATAGCATGCCTAGCTATTATGT	1056	

RESULT 12

BU365958	774 bp	linear	EST 28-NOV-2002
LOCUS	BU365958	mRNA	
DEFINITION	603785840F1 CSEQCHN72	Gallus gallus	clone CHEST741p10 5', mRNA sequence.

ACCESSION

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
B036938	B036998.1	GI:25873959	Gallus gallus (chicken)	
	EST.		Gallus gallus	
			Gallus gallus	
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
			Archosauria; Aves; Neognathae; Galliformes; Phasianidae;	
			Phasianinae; Gallus.	

REFERENCE

AUTHORS	Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken CDNAS
TITLE	Curr. Biol. 12 (22), 1965-1969 (2002)
JOURNAL	22335534
MEDLINE	12445392
PUBMED	12445392
COMMENT	Contact: Simon Hubbard

COMMENT

Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

```

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/db_xref="taxon:9031"
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/clone_lib="CSQCCHN72"
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constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

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ORIGIN

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Db 10 TCCAGCTGGGAGAGTGTTCACCTGTCTCCACCCCTGTGGCCGAGGCTGGCAGAGGCG 69
QY 21 SerArgSerCysThrAsnProAlaProLeuAenGlyAlaPheCysGluGlyGlnAen 40
Db 70 ACCCGGACCTGCACCAACCCCGCTCCACTCAACGAGGGGCGCTTCTGCGAGGGCCAGGCA 129
QY 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 130 TTCCAGAGAGCGCGCTGCACCAACCATCTGC 159

RESULT 15
LOCUS BX920046/c
DEFINITION BX920046 Sus Scrofa library (scan) Sus scrofa cDNA clone
scan0009d.p.02 5prim, mRNA sequence.

ACCESSION BX920046
VERSION BX920046.1 GI:41136865
KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

TITLE Bonnet,A., Tosser-Klopp,G., Benne,P., Cabau,C., Villegier,S.,

JOURNAL A Pig Normalised Multi-Tissue cDNA Library

COMMENT Unpublished (2003)

Contact: Tosser-Klopp G

Institut National de la Recherche Agronomique

Chemin de Borde-Rouge - Auzerville BP27, 31326 Castanet-Tolosan

cedex, FRANCE

Tel: 33 (0) 5.61.28.51.14

Fax: 33 (0) 5.61.28.53.08

Email: tosser@toulouse.inra.fr

Sequence cleaned of vector, adaptor and repetitions. Contact us
at signenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.

Plate: 0009 row: p column: 2.

FEATURES

source

Location/Qualifiers

1..733

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/mol_type="mRNA"

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/clone="scan0009d.p.02"

/tissue type="mixed"

/dev stages="from embryos to adults"

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skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo urethral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"

ORIGIN

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Db 418 TCCCGGACCTGCACCAATCCAGCTCCTCTCAATGTTGGGGCCTTTTGTGAGGGATGTCA 359
QY 41 ValGlnLysThrAlaCysAlaThrLeuCys 50
Db 358 GTGCAGAAAATAACCTGCACCTTCTCTCTGT 329

Search completed: September 9, 2005, 04:40:42
Job time : 1648.59 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:47:02 ; Search time 747.981 Seconds
(without alignments)
1166.064 Million cell updates/sec

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Perfect score: 86
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Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: gb.pat.*
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8: gb.pl.*
9: gb.pr.*
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11: gb.sts.*
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13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	86	100.0	813 AX054892 Sequence
3	86	100.0	1787 BD057525 Netrin re
4	86	100.0	2688 BC009333 Homo sapi

5	86	100.0	2697	6	AX451652	Sequence
6	86	100.0	2752	6	AX449572	Sequence
7	86	100.0	2784	6	CQ730306	Sequence
8	86	100.0	2881	6	AX527916	Sequence
9	86	100.0	3580	6	AX367094	Sequence
10	86	100.0	121282	9	AC027318	Homo sapi
c 11	86	100.0	166534	2	AC034209	Homo sapi
c 12	86	100.0	168168	2	AC012283	Homo sapi
c 13	83	96.5	3844	10	BC058084	Mus muscu
c 14	83	96.5	3992	10	MMU487852	Mus muscu
c 15	83	96.5	4294	10	AK122575	Mus muscu
c 16	83	96.5	242128	2	AC123700	Mus muscu
c 17	82	95.3	349	6	BD204134	5' EST and
c 18	68	79.1	2697	6	AX268596	Sequence
c 19	68	79.1	2697	10	RNU87305	U7305 Rattus norv
c 20	68	79.1	3014	6	BD057524	Netrin re
c 21	68	79.1	171419	2	AC135142	Rattus no
c 22	68	79.1	231407	2	AC139592	Rattus no
c 23	60	69.8	184142	10	AC132356	Mus muscu
c 24	60	69.8	213047	2	AC099622	Mus muscu
c 25	59	68.6	174558	10	AC132092	Mus muscu
c 26	58	67.4	3743	8	BT003880	Arabidops
c 27	58	67.4	5520	6	AX046187	Sequence
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c 32	58	67.4	223446	2	AC098637	Rattus no
c 33	58	67.4	231933	2	AC113817	Rattus no
c 34	58	67.4	234234	2	AC097194	Rattus no
c 35	58	67.4	252127	2	AC108230	Rattus no
c 36	58	67.4	257679	2	AC134801	Rattus no
c 37	58	67.4	264875	2	AC107101	Rattus no
c 38	57	66.3	247780	2	AC106305	Rattus no
c 39	56	65.1	441	11	G67418	Hal796-ar S
c 40	56	65.1	851	6	BD092428	Identific
c 41	56	65.1	1024	6	AX787900	Sequence
c 42	56	65.1	10860	1	AE000589	Helicobac
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c 44	56	65.1	66054	2	CEY102G3	Continuation (4 of
c 45	56	65.1	122592	3	CEY60A3A	AL117207 Caenorhab

ALIGNMENTS

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DEFINITION	AX451656	Sequence 5 from Patent WO0233080.				
ACCESSION	AX451656					
VERSION	AX451656.1	GI:21698589				
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1	Koehler, R.H.				
AUTHORS		Regulation of human netrin binding membrane receptor unc5h-1				
TITLE		Patent: WO 0233080-A 5 25-APR-2002;				
JOURNAL		Bayer Aktiengesellschaft (DE)				
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FEATURES

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Db	1203	CTGTCTCTGTCGTCTGTCCTCAICTCGTTATTCGCCGAAGAGGGGG	1256	
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LOCUS	AX367094	3580 bp	DNA	linear PAT 16-FEB-2002
DEFINITION	Sequence 13 from Patent WO0198354.			
ACCESSION	AX367094			
VERSION	AX367094.1	GI:18855296		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1	Griffin,J.A., Kallick,D.A., Tribouley,C.M., Yue,H., Nguyen,D.B.,		
AUTHORS	Tang,Y.T., Lal,P., Policky,J.L., Azimzai,X., Lu,D.A., Graul,R.,			
	Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O.,			
	Patterson,C., Yang,J., Xu,Y., Warren,B.A., Ding,L. and			
	Sanjanwala,M.S.			
TITLE	Receptors			
JOURNAL	Patent: WO 0198354-A 13 27-DEC-2001;			
	Incyte Genomics, Inc. (US)			
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ACCESSION	AC027318			
VERSION	AC027318.5	GI:25989047		
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ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1	(bases 1 to 121282)		
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.			
JOURNAL	Direct Submission			
TITLE	Unpublished			
REFERENCE	2	(bases 1 to 121282)		
AUTHORS	DOE Joint Genome Institute.			
TITLE	Direct Submission			
JOURNAL	Submitted (30-MAR-2000) Production Sequencing Facility, DOE Joint			
REFERENCE	Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA			
AUTHORS	DOE Joint Genome Institute.			

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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 20:54:46 ; Search time 93.0905 Seconds
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Scoring table: BLOSUM62
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	86	100.0	604	6 ABK52893	ABK52893 Human net
3	86	100.0	813	4 AAC90917	AAC90917 Human UNC
4	86	100.0	1009	12 ADH71615	ADH71615 Human gen
5	86	100.0	1787	2 AAV52941	AAV52941 Human UNC

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XX	AAH99392	
AC	AAH99392	
XX	16-OCT-2001	(first entry)
DT	16-OCT-2001	(first entry)
XX	Human protein encoding cDNA sequence SEQ	
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DE	antiflamatory; antirheumatic; antiarthr	
KW	antibacterial; endocrine; cardiac; centr	
KW	anti-HIV; fungicide; antimutagen; cardio	
KW	anti-aggregant; haemostatic; vulnerar; an	
KW	dermatological; antiallergic; antiasthma	
KW	neuroprotective; antidepressant; nootropi	
KW	immunostimulant; gene therapy; antise	
KW	anti-anaphylactic; rheumatoid arthritis; s	
KW	cardiac dysfunction; neuropathology; card	
KW	genetic disease; haematopoietic disorder;	
KW	thrombocytopenia; osteoporosis; severe c	
KW	allergic rhinitis; diabetes; multiple scl	
KW	Alzheimer's disease; Parkinson's disease;	
KW	neurological disorder; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200153455-A2.	

ALIGNMENTS

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RESULT 6

ADH71623

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XX AC ADH71623;

XX DT 25-MAR-2004 (first entry)

XX DE Human gene of the invention NOV21h SEQ ID NO:519.

XX KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; neurotropic; anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy; KW cancer; cachexia; Alzheimer's disease; Parkinson's disease; KW obesity; diabetes; infectious disease; metabolic syndrome X; KW dyslipidaemia.

XX OS Homo sapiens.

XX PN WO2003102155-A2.

XX PD 11-DEC-2003.

XX PF 03-JUN-2003; 2003WO-US017430.

XX 03-JUN-2002; 2002US-0385120P.

PR 04-JUN-2002; 2002US-0385784P.

PR 05-JUN-2002; 2002US-0386041P.

PR 05-JUN-2002; 2002US-0386047P.

PR 06-JUN-2002; 2002US-0386376P.

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PR 06-JUN-2002; 2002US-0387016P.

PR 07-JUN-2002; 2002US-0386796P.

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PR 08-JUN-2002; 2002US-0296960P.

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PR 18-JUN-2002; 2002US-0389884P.

PR 19-JUN-2002; 2002US-0390006P.

PR 19-JUN-2002; 2002US-0390209P.

PR 21-JUN-2002; 2002US-0390763P.

PR 17-JUL-2002; 2002US-0396706P.

PR 06-AUG-2002; 2002US-0401628P.

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PR 09-AUG-2002; 2002US-0402389P.

PR 12-AUG-2002; 2002US-0402786P.

PR 12-AUG-2002; 2002US-0402816P.

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PR 13-AUG-2002; 2002US-0406317P.

PR 15-AUG-2002; 2002US-0403617P.

PR 26-AUG-2002; 2002US-0406182P.

PR 26-AUG-2002; 2002US-0406355P.

PR 27-AUG-2002; 2002US-0406240P.

PR 12-SEP-2002; 2002US-0410084P.

PR 20-SEP-2002; 2002US-0412528P.

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PR 28-OCT-2002; 2002US-0421156P.

PR 31-OCT-2002; 2002US-0422690P.

PR 01-NOV-2002; 2002US-0423130P.

PR 05-NOV-2002; 2002US-00423798.

PR 05-NOV-2002; 2002US-0423798P.

PR 12-NOV-2002; 2002US-0425453P.

XX (CURA-) CURAGEN CORP.

XX PA

XX Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ; Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K; Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X; Gusev VI, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, MacDougall JR; Maclachlan T, Malyankar UM, Mexick AJ, Millet I, Mishra VS; Padiguru M, Patturajan M, Pena CEA, Feyman JA, Raha D, Rastelli L; Rieger DK, Rothenberg ME, Sciore P, Shency SG, Shinkets RA; Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M; Zhong H;

XX WPI; 2004-081935/08.

DR P-PSDB; ADH71624.

XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or treating NOVX-associated disorders, e.g. cancer, diabetes, infection or obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

PT

XX Example 21; SEQ ID NO 519; 1880pp; English.

PS

XX The invention relates to a novel isolated polypeptide (NOVX). A polypeptide of the invention has cytostatic, immunomodulator, neuroprotective, neurotropic, anorectic, antidiabetic, antimicrobial, and antilipemic activity, and may have a use in gene therapy, and as a vaccine. The polypeptides are encoded by NOVX polynucleotides comprising any of the 303 fully defined nucleotide sequences given in the specification. The polypeptide is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The polypeptide, polynucleotide and antibody are useful in diagnosing, treating or preventing NOVX-associated disorders, e.g. cancer, cachexia, Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue CC typing, preventive medicine, and pharmacogenomics. The present sequence CC encodes a NOVX polypeptide of the invention.

XX

SQ Sequence 2463 BP; 470 A; 828 C; 721 G; 444 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.00268 Length: 2463

Score: 86.00 Matches: 18

Percent Similarity: 100.00% Conservative: 0

XX Human gene of the invention NOV21m SEQ ID NO:529.
DE ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX Homo sapiens.
OS W02003102155-A2.
XX 11-DEC-2003.
XX 03-JUN-2003; 2003WO-US017430.
XX 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 07-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0387296P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0387626P.
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PR 11-JUN-2002; 2002US-0387625P.
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PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
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PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389118P.
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PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 09-AUG-2002; 2002US-0401566P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
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PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
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PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
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PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
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PR 09-OCT-2002; 2002US-0417186P.
PR 23-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX (CURA-) CURAGEN CORP.
XX Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
XX Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Eitenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Guev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Macleachlan T, Malyankar UM, Mezick AU, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Raetelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
XX Zhong H;
XX WPI; 2004-081935/08.
DR P-PSDB; ADH71634.
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
XX treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
XX obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX Example 21; SEQ ID NO 529; 1880pp; English.
XX The invention relates to a novel isolated polypeptide (NOVX). A
XX polypeptide of the invention has cytostatic, immunomodulator,
XX neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
XX antilipaeamic activity, and may have a use in gene therapy, and as a
XX vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
XX any of the 303 fully defined nucleotide sequences given in the
XX specification. The polypeptide is useful in the manufacture of a
XX medicament for treating a syndrome associated with a human disease. The
XX polypeptide, polynucleotide and antibody are useful in diagnosing.
XX treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
XX Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
XX diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
XX further used as hybridisation probes, in chromosome mapping, tissue
XX typing, preventive medicine, and pharmacogenomics. The present sequence
XX encodes a NOVX polypeptide of the invention.
SQ Sequence 2880 BP; 527 A; 984 C; 867 G; 502 T; 0 U; 0 Other;
Alignment Scores:
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Score: 86.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Db 1202 CTGGTCCTGCTGCTGCTTGTCTCATCTCTGTTTATTGCGGAGAGAGGGG 1255

ID	ADG42568 standard; CDNA; 2881 BP.
XX	
AC	ADG42568;
DT	26-FEB-2004 (first entry)
DE	Novel human NOV1 cDNA.
KW	cytostatic; gene therapy; NOXV-agonist; NOXV-antagonist; pharmaceutical;
OS	NOXV-associated disorder; cancer; human; gene; ss.
FN	Homo sapiens.
PD	US2003204052-A1.
PP	30-OCT-2003 .
PR	04-OCT-2001; 2001US-00970944 .
PT	04-OCT-2000; 2000US-0237862P.
PI	(HERR/) HERRMANN J L.
PA	(RAST/) RASTELLI L.
SH	(SHIM/) SHINKETS R A.
PL	Herrmann JL, Rastelli L, Shinkets RA;
DR	WPI; 2003-900673/82.
P-PSDB	P-PSDB; ADG42569.
PT	New NOXV gene or NOXV-specific antibody, useful for preparing a
FT	composition for treating or preventing a NOXV-associated disorder, e.g.,
PT	cancer.
PS	Claim 9; SEQ ID NO 1; 118pp; English.
CC	The invention describes a new isolated polypeptide comprising: a
CC	polypeptide or its mature form comprising a sequence not given in the
CC	specification; or a variant of (A), where one or more amino acid residues
CC	in the variant differs in no more than 15% from the amino acid sequence
CC	of the mature form. The pharmaceutical composition may be administered
CC	via oral, transdermal, rectal or parenteral route. The polypeptide,
CC	nucleic acid or antibody is useful for preparing a composition for
CC	treating or preventing a NOXV-associated disorder, e.g., cancer. This
CC	sequence encodes a human NOXV protein.
SQ	Sequence 2881 BP; 526 A; 987 C; 866 G; 502 T; 0 U; 0 Other;
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ID	ADH71649 standard; DNA; 2881 BP.
XX	
AC	ADH71649;
DT	25-MAR-2004 (first entry)
XX	
DB	Human gene of the invention NOV21u SEQ ID NO:545.
XX	

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ID	ABK49422 standard; DNA; 2881 BP.
XX	
AC	ABK49422;
DT	15-JUL-2002 (first entry)
DE	DNA encoding human UNC5-like protein NOV1.
KW	Human; NOXV polypeptide; cardiomyopathy; atherosclerosis; cancer;
OS	cell signal processing; metabolic pathway modulation; cancerous tissue;
FN	antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;
PD	chromosome 13; gene; ds.
OS	Homo sapiens.
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FT	/product= "Human UNC5-like protein NOV1"
WO200229038-A2.	
11-APR-2002.	
04-OCT-2001; 2001WO-US031377.	
04-OCT-2000; 2000US-0237862P.	
(CURA-) CURAGEN CORP.	
Herrmann JL, Rastelli L, Shinkets RA;	
P-PSDB; AAU79939.	
Noxv isolated NOXV polypeptide, and encoded polynucleotide, useful for	
treating cardiomyopathy, atherosclerosis, and cancer.	
Claim 8; Page 7-8; 180pp; English.	
The present invention relates to a new NOXV polypeptide having a 900	
(NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)	
residue amino acid sequence, as given in the specification. The novel	
polypeptide, and its encoding polynucleotide, are used to treat	
cardiomyopathy, atherosclerosis, cancer or a disease related to cell	
signal processing and metabolic pathway modulation, in a human. Detecting	
the polypeptide or polynucleotide is useful for identifying cancerous	
tissue. The antibody can be used to treat diabetes or cancer. The host	
cells can be used to produce non-human transgenic animals useful in drug	
screening. The present nucleic acid sequence is that of the human UNC5-	
like NOV1 gene located on chromosome 13. This sequence encodes the human	
UNC5-like protein NOV1 of the invention	
Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;	
Alignment Scores:	
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Copyright (c) 1993 - 2005 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	68	79.1	3014	2	US-08-808-982-1
5	68	79.1	3014	3	US-09-308-902A-1
6	52	60.5	3111	2	US-09-014-969-12
7	52	60.5	3881	4	US-09-774-528-139
8	51	59.3	1410	4	US-09-270-767-13235
9	51	59.3	138282	4	US-09-949-016-15307
10	49	57.0	866	4	US-09-629-222A-44
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12	49	57.0	1854	1	US-08-249-420-1

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c 16	48.5	56.4	601	4	US-09-949-016-117417	Sequence 117417, A
c 17	48.5	56.4	601	4	US-09-949-016-117418	Sequence 117418, A
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c 19	48.5	56.4	114842	4	US-09-949-016-14993	Sequence 14993, A
c 20	48	55.8	201	4	US-09-248-796A-9121	Sequence 9121, Ap
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c 24	48	55.8	7475	2	US-08-971-036-1	Sequence 1, Appli
c 25	48	55.8	7475	3	US-08-056-570-1	Sequence 1, Appli
c 26	48	55.8	7475	3	US-09-265-017B-1	Sequence 1, Appli
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c 45	47	54.7	601	4	US-09-949-016-61325	Sequence 61325, A

ALIGNMENTS

RESULT 1
US-08-808-982-2
; Patent No. 5939271
; Sequence 2, Application US/08808982

GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:


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; REFERENCE/DOCKET NUMBER.: UC96-217
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 3014 base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: double
;         TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-306-902A-1

Alignment Scores:
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Best Local Similarity: 77.78% Mismatches: 3
Query Match: 79.07% Indels: 0
DB: 3 Gaps: 0

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Qy 1 LeuValLeuLeuLeuValLeuValLeuValTyCysArgLysLeuGly 18
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RESULT 6
US-09-014-969-12
; Sequence 12, Application US/09014969
; Patent No. 5965397
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Racie, Lisa A.

APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.

TITLE OF INVENTION: ENCODING THEM
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 Cambridgepark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/014,969
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sprunger, Suzanne A.
 REGISTRATION NUMBER: 41,323
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-8284
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 12:
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 LENGTH: 311 base pairs
 TYPE: nucleic acid
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 TOPOLOGY: linear
 MOLECULE TYPE: cDNA


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; PRIOR APPLICATION NUMBER: 09/463,891
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US98/15828
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/053,936
; PRIOR FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 866
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-629-222A-44

Alignment Scores:
Pred. No.:      47.7      Length:      866
Score:          49.00     Matches:      10
Percent Similarity: 80.00% Conservative:    2
Best Local Similarity: 66.67% Mismatches:      3
Query Match:    56.98% Indels:              0
DB:            4        Gaps:              0

US-10-624-932C-2_COPY_372_389 (1-18) x US-09-629-222A-44 (1-866)
Qy   1 LeuValLeuLeuValLeuValLeuValTyrCysArgLys 15
Db   87 CTTTCCTTAAGCCTGAAGATTTAAATTACTGTACTGCCGAAAG 131

RESULT 11
US-09-629-222A-5
; Sequence 5, Application US/09629222A
; Patent No. 6599700
; GENERAL INFORMATION:
; APPLICANT: Bellacosa, Alfonso
; TITLE OF INVENTION: Methods for Detection of Transition
; FILE REFERENCE: FCCC 96-21
; CURRENT APPLICATION NUMBER: US/09/629,222A
; CURRENT FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/463,891
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US98/15828
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/053,936
; PRIOR FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1514
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-629-222A-5

Alignment Scores:
Pred. No.:      95.2      Length:      1514
Score:          49.00     Matches:      10
Percent Similarity: 80.00% Conservative:    2
Best Local Similarity: 66.67% Mismatches:      3
Query Match:    56.98% Indels:              0
DB:            4        Gaps:              0

US-10-624-932C-2_COPY_372_389 (1-18) x US-09-629-222A-5 (1-1514)
Qy   1 LeuValLeuLeuValLeuValLeuValTyrCysArgLys 15
Db   289 CTTTCCTTAAGCCTGAAGATTTAAATTACTGTACTGCCGAAAG 333

RESULT 12
US-08-249-420-1
; Sequence 1, Application US/08249420
; Patent No. 5484724
; GENERAL INFORMATION:
; APPLICANT: El-Sherbeini, Mohamed
; TITLE OF INVENTION: DNA ENCODING GLS1
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christine E. Carty
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,420
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Carty, Christine E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19162
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1854 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-249-420-1

Alignment Scores:
Pred. No.:      122      Length:      1854
Score:          49.00     Matches:      8
Percent Similarity: 87.50% Conservative:    6
Best Local Similarity: 50.00% Mismatches:      2
Query Match:    56.98% Indels:              0
DB:            1        Gaps:              0

US-10-624-932C-2_COPY_372_389 (1-18) x US-08-249-420-1 (1-1854)
Qy   3 LeuLeuLeuValLeuValLeuValTyrCysArgLysGlugly 18
Db   1714 CTATTGTACTATTACATCACTATTATTATTATAAAGACCGATGGT 1761

RESULT 13
US-08-737-663-1
; Sequence 1, Application US/08737663
; Patent No. 5955337
; GENERAL INFORMATION:
; APPLICANT: El-Sherbeini, Mohamed
; TITLE OF INVENTION: DNA ENCODING GLS1
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joseph A. Coppola - MERCK & CO., INC.
; STREET: 126 E. Lincoln Avenue - P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,663

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 9, 2005, 04:41:16 ; Search time 179.624 Seconds
(without alignments)
658.098 Million cell updates/sec

Title: US-10-624-932c-2_COPY_372_389
Perfect score: 86
Sequence: 1 LVLLLLLVLLVYCRKKG 18

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HCAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -WAP=US10624932 @cgn 1 1 989 @runat 08092005_161709_15882
-NCPU=6 -ICPU=3 -NO MMAR -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Published Applications NA:
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq*
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*
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 - 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
 - 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
 - 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
 - 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
 - 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
 - 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
 - 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
 - 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
 - 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
 - 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*
 - 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq*
 - 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq*
 - 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq*
 - 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq*
 - 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
 - 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq*
 - 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
 - 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
 - 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	390	18	US-10-296-115-227
2	86	100.0	1787	10	US-09-933-261-2
3	86	100.0	1787	14	US-10-256-702-2
4	86	100.0	2752	18	US-09-918-779-1
5	86	100.0	2752	18	US-10-624-932-1
6	86	100.0	2881	10	US-09-970-944-1
7	86	100.0	3561	20	US-10-643-795A-77
8	86	100.0	3561	21	US-10-948-518-77
9	86	100.0	3580	17	US-10-311-623-13
c 10	86	100.0	9582	9	US-09-764-861-62
c 11	86	100.0	9582	10	US-09-764-861-62
c 12	86	100.0	9582	14	US-10-115-928-62
c 13	86	100.0	18772	9	US-09-764-861-63
c 14	86	100.0	18772	10	US-09-764-861-63
c 15	86	100.0	18772	14	US-10-115-928-63
c 16	82	95.3	349	21	US-10-926-683-345
c 17	68	79.1	2697	16	US-10-240-154-15
c 18	68	79.1	3014	10	US-09-933-261-1
c 19	68	79.1	3014	14	US-10-256-702-1
c 20	56	65.1	851	9	US-09-895-913A-47
c 21	54	62.8	1587	18	US-10-425-114-14571
c 22	54	62.8	1875	20	US-10-739-930-939
c 23	53	61.6	225	17	US-10-242-535A-14360
c 24	53	61.6	225	18	US-10-085-783A-14360
c 25	53	61.6	327	19	US-10-674-124A-5507
c 26	53	61.6	403	18	US-10-424-599-43127
c 27	53	61.6	1594	9	US-09-823-245A-412
c 28	53	61.6	2066	21	US-10-764-420-2078
c 29	53	61.6	3015	19	US-10-033-388-1
c 30	53	61.6	18605	14	US-10-057-726-17
c 31	53	61.6	18855	15	US-10-311-455-584
c 32	53	61.6	20083	20	US-10-723-860-3920
c 33	53	61.6	2731748	19	US-10-297-465A-1
c 34	52	60.5	843	17	US-10-369-493-46895
c 35	52	60.5	978	19	US-10-437-963-49300
c 36	52	60.5	2579	19	US-10-437-963-40594
c 37	52	60.5	3518	17	US-10-437-963-49301
c 38	52	60.5	3881	17	US-10-120-988-139
c 39	52	60.5	3958	17	US-10-172-118-263
c 40	52	60.5	3958	18	US-10-342-887-263
c 41	52	60.5	3958	22	US-10-756-149-520
c 42	51	59.3	218	19	US-10-674-124A-26691
c 43	51	59.3	287	19	US-10-674-124A-13058
c 44	51	59.3	449	19	US-10-674-124A-16394
c 45	51	59.3	643	13	US-10-027-632-47786

ALIGNMENTS

RESULT 1

US-10-296-115-227
; Sequence 227, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296.115
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488.725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552.317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 227

[illegible]

Alignment Scores:	
Pred. No.:	0.00335
Score:	86.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	10
Length:	2752
Matches:	18
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

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Qy 1 LeuValLeuLeuLeuValLeuIleLeuValTyrCysArgLysLysGluGly 18
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Dd 1159 CTGGTCCTGCTGCTGTGCCTCATCTCGTTATTGCCGGAGAAGAGGGG 1212

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RESULT 5
US-10-624-932-1
; Sequence 1, Application US/10624932
; Publication No. US20040096977A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muradidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shinkete, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Zyrtek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsobrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: Novel Proteins
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/10/0-71
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918, 7
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221, 4
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222, 8
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223, 7
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223, 7
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223, 7
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225, 1
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225, 3
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225, 4
; PRIOR FILING DATE: 2000-08-15
; Remaining Prior Application data r
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-624-932-1

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Alignment Scores:		
Pred. No.:	0.00335	Length:
Score:	86.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	100.00%	Indels:
DB:	18	Gaps:
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		18

US-10-624-932C-2 COPY 372 389 (1-18) x US-10-624-932-1 (1-2752)

Qy 1 LeuValLeuLeuLeuValLeuLeuLeuValTyrCysArgLysLysGluGly 18
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Db 1159 CTGGTCCTGCTGCTGTGTCTCATCTCTCGTATTGCGGAGAAGAGAGGG 1212

RESULT 6
US-09-970-944-1

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; Sequence 1, Application US/09070944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shinkets, Richard A
; TITLE OF INVENTION: No. US20030204
; TITLE OF INVENTION: No. US20030204
; TITLE OF INVENTION: Antibodies Di
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,8
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2881
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-944-1

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Alignment Scores:		
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Score:	86.00	Matches: 18
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	10	Gaps: 0

US-10-624-932C-2 COPY 372 389 (1-18) x US-09-970-944-1 (1-2881)

Qy 1 LeuValIleuLeuLeuValIleLeuValTyrCysArgLysLysGluGly 18
| | | | | | | | | | | | | | | | | | | |
Dp 1203 CTGGTCCTGCTGCTGTCTCATCTCGTTATTGCCGGAAGAAGAGGG 1256
| | | | | | | | | | | | | | | | | | | |

RESULT 7

US-10-643-795A-77
 ; Sequence 77, Application US/10643795A
 ; Publication No. US20040241703A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FREDERIC J. DESAUVAGE
 ; APPLICANT: GRETCHEN FRANTZ
 ; APPLICANT: KENNETH J. HILLAN
 ; APPLICANT: PAUL POLAKIS
 ; APPLICANT: ANDREW POLSON
 ; APPLICANT: VICTORIA SMITH
 ; APPLICANT: SUSAN D. SPENCER
 ; APPLICANT: THOMAS D. WU
 ; APPLICANT: ZEMIN ZHANG

TITLE OF INVENTION:	COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION:	TREATMENT OF TUMOR
FILE REFERENCE:	P5026R1-US
CURRENT APPLICATION NUMBER:	US 10/643,795A
CURRENT FILING DATE:	2003-08-19
PRIOR APPLICATION NUMBER:	US 60/404,809
PRIOR FILING DATE:	2003-08-19
PRIOR APPLICATION NUMBER:	US 60/405,645
PRIOR FILING DATE:	2003-08-21
PRIOR APPLICATION NUMBER:	US 60/413,192
PRIOR FILING DATE:	2002-09-23
PRIOR APPLICATION NUMBER:	US 60/419,008
PRIOR FILING DATE:	2002-10-15
PRIOR APPLICATION NUMBER:	US 60/426,847
PRIOR FILING DATE:	2002-11-15
PRIOR APPLICATION NUMBER:	US 60/484,959
PRIOR FILING DATE:	2003-07-02
NUMBER OF SEQ ID NOS:	158

LENGTH: 3561

; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-643-795A-77

Alignment Scores:

Pred. No.:	0.00459	Length:	3561
Score:	86.00	Matches:	18
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-10-624-932C-2 COPY 372 389 (1-18) x US-10-643-795A-77 (1-3561)

QY	1	Leu	Val	Leu	Leu	Val	Leu	Ile	Leu	Val	Tyr	Cys	Arg	Lys	Lys	Glu	Gly	18
Db	949	CTGGT	CCT	GTG	CTG	TGT	CTCT	CACT	CCT	CGT	TTATT	TTC	CCG	GAG	AAG	AGG	GGG	1002

RESULT 8

US-10-948-518-77
; Sequence 77, Application US/10948518
; Publication No. US20050064492A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: TEMIN ZHANG

1 APPLICANT: ZEMIN ZHANG
 2 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
 3 TREATMENT OF TUMOR
 4 FILE REFERENCE: P5026R1-US
 5 CURRENT APPLICATION NUMBER: US/10/948,518
 6 CURRENT FILING DATE: 2004-09-22
 7 PRIOR APPLICATION NUMBER: US/10/643,795
 8 PRIOR FILING DATE: 2003-08-19
 9 PRIOR APPLICATION NUMBER: US 60/404,809
 10 PRIOR FILING DATE: 2002-08-19
 11 PRIOR APPLICATION NUMBER: US 60/405,645
 12 PRIOR FILING DATE: 2002-08-21
 13 PRIOR APPLICATION NUMBER: US 60/413,192
 14 PRIOR FILING DATE: 2002-09-23
 15 PRIOR APPLICATION NUMBER: US 60/419,008
 16 PRIOR FILING DATE: 2002-10-15
 17 PRIOR APPLICATION NUMBER: US 60/426,847
 18 PRIOR FILING DATE: 2002-11-15
 19 PRIOR APPLICATION NUMBER: US 60/484,959
 20 PRIOR FILING DATE: 2003-07-02
 21 NUMBER OF SEQ ID NOS: 158

LENGTH: 3561

; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-948-518-77

Alignment Scores:

Assignment Score:	0.00459	Length:	3561
Pred. No.:	86.00%	Matches:	18
Score:	100.00%	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
DB:	21		

US-10-624-932C-2 COPY 372 389 (1-18) x US-10-948-518-77 (1-3561)

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pb 949 CTGGTCCTGCTGCTGTGCTCACTCTCGTTATTGCCGGAAGAAGGGGG 1002

RESULT 9

US-10-311-623-13
; Sequence 13, Application US/10311623
; Publication No. US20040023244A1
; GENERAL INFORMATION:


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RESULT 10
US-09-764-861-62/c
; Sequence 62, Application US/09764861
; Publication No. US20020086811A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204
; CURRENT APPLICATION NUMBER: US/09/764,861
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 9582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-861-62

Alignment Scores:
Pred. No.: 0.0155 Length: 9582
Score: 86.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0

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; FILE REFERENCE: P7204C1
; CURRENT APPLICATION NUMBER: US/10/115,928
; CURRENT FILING DATE: 2002-04-05
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 9582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-115-928-62

Alignment Scores:
Pred. No.: 0.0155 Length: 9582
Score: 86.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x US-10-115-928-62 (1-9582)
Oy 1 LeuValLeuLeuValLeuValLeuValTyrCysArgJysbysG

```


GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 22:38:37 ; Search time 592.413 Seconds
(without alignments)
1156.553 Million cell updates/sec

Title: US-10-624-932c-2_COPY_372_389
Perfect score: 86
Sequence: 1 LVLLLVLLVYCRKKG 18

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2.1/USPTO spool h/US10624932/runat_08092005_161706_15792/app_query.fasta_1.1386
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.coi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10624932 @CGN 1 1 8180 @runat_08092005_161706_15792 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	604	2 BE314370	BE314370 601147261
2	86	100.0	859	2 BF311896	BF311896 601897733
3	86	100.0	934	2 BF311804	BF311804 601897316
4	86	100.0	1532	3 BC033727	BC033727 Homo sapi
5	83	96.5	501	7 CN691436	CN691436 E0309E05-
6	83	96.5	548	4 BI900830	BI900830 ib81g04.y
7	83	96.5	675	6 CA315487	CA315487 UI-M-FW0
8	83	96.5	723	5 BU613458	BU613458 UI-M-FW0
9	83	96.5	756	5 BU612387	BU612387 UI-M-EW0

10	83	96.5	788	6	CA317532	CA317532 UI-M-FW0-	
11	72	83.7	872	7	CF585872	CF585872 AGENCOURT	
12	70	81.4	608	4	BM487397	BM487397 pgm2n.pk0	
13	66	76.7	514	5	BX522364	BX522364 BX522364	
14	66	76.7	815	7	CK140529	CK140529 AGENCOURT	
15	65	75.6	531	8	BH657369	BH657369 BOMFY84TF	
c	16	65	75.6	683	8	BH963887	BH963887 odh84e02..
17	65	75.6	789	8	BZ445020	BZ445020 BONMX88TF	
18	60	69.8	560	1	AI558191	AI558191 vk25f10.y	
19	60	69.8	572	1	AA543602	AA543602 vk25f10.y	
20	58	67.4	405	9	CNS00XJG	AL094954 Arabidops	
21	58	67.4	676	3	CNS08LLI	BX017410 Single re	
22	58	67.4	1008	3	CNS08VZJ	BX030875 Single re	
c	23	56	65.1	243	8	AZ762451	AZ762451 IM0557P09
c	24	56	65.1	379	7	CV184054	CV184054 tai91a12.
25	56	65.1	459	8	BZ674458	BZ674458 PUBX86TD	
c	26	56	65.1	547	7	CO371148	CO371148 tah70g05.
c	27	56	65.1	580	5	BP505476	BP505476 BP505476
c	28	56	65.1	659	8	CC165132	CC165132 1189c09.b
c	29	56	65.1	743	8	BZ822958	BZ822958 PUFAY31TD
30	56	65.1	776	8	BZ822956	BZ822956 PUFAY31TB	
31	56	65.1	812	9	CC661906	CC661906 OGUDY06TV	
32	56	65.1	814	8	AQ411942	AQ411942 CPG0921B	
c	33	56	65.1	841	7	CV180913	CV180913 tai85a08.
c	34	56	65.1	858	9	CC682181	CC682181 OG0BM86TH
c	35	56	65.1	917	9	CNS07DXS	AL441062 T7 end of
c	36	56	65.1	920	9	CG276138	CG276138 OG3AG23TV
c	37	56	65.1	938	9	CNS07D8D	AL440147 T7 end of
38	56	65.1	1009	5	BU857896	BU857896 AGENCOURT	
39	55	64.0	236	1	AV252353	AV252353 AV252353	
40	55	64.0	416	6	CD586290	CD586290 RK035A350	
41	55	64.0	552	9	TA232602P	AL481052 T. brucei	
42	55	64.0	582	5	BX872954	BX872954 BX872954	
43	55	64.0	587	5	BX911995	BX911995 BX911995	
c	44	55	603	7	CN748091	CN748091 SAL US004	
c	45	55	684	9	CE274919	CE274919 tigr-g88-	

ALIGNMENTS

RESULT 1
BE314370
LOCUS BE314370 604 bp mRNA linear EST 26-OCT-2000
DEFINITION 601147261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3162710 5',
mRNA sequence.
ACCESSION BE314370
VERSION BE314370.1 GI:9135413
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 604)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCMI22 row: i column: 15
High quality sequence stop: 601.
Location/Qualifiers
1..604
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3162710"
/tissue_type="neuroblastoma"

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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 0.00252 Length: 604
Score: 86.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x BE314370 (1-604)

Qy 1 LeuValLeuLeuValLeuValLeuValTyrcysArgLysGluGly 18
|||||
Db 25 CTGGTCTGCTGCTGCTGCTCATCTCTGTTATTGCGGAGAGAGAGGGG 78

RESULT 2
BF311896 601897733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126760 5',
LOCUS mRNA sequence.
ACCESSION BF311896.1 GI:11259667
VERSION BF311896.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMI017 row: b column: 09
High quality sequence stop: 684.
Location/Qualifiers
1. 859
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4126760"
/tissue_type="neuroblastoma"
/lab_host="NIH_MGC_19"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

FEATURES
source
1. 859
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4126760"
/tissue_type="neuroblastoma"
/lab_host="NIH_MGC_19"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 0.00369 Length: 859
Score: 86.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x BF311804 (1-934)

Qy 1 LeuValLeuLeuValLeuValLeuValTyrcysArgLysGluGly 18
|||||
Db 45 CTGGTCTGCTGCTGCTGCTCATCTCTGTTATTGCGGAGAGAGGGG 98

RESULT 4
BC033727

```

```

Score: 86.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x BF311896 (1-859)

Qy 1 LeuValLeuLeuValLeuValLeuValTyrcysArgLysGluGly 18
|||||
Db 44 CTGGTCTGCTGCTGCTGCTCATCTCTGTTATTGCGGAGAGAGGGG 97

RESULT 3
BF311804 601897731F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126706 5',
LOCUS mRNA sequence.
ACCESSION BF311804
VERSION BF311804.1 GI:11259566
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMI016 row: p column: 03
High quality sequence stop: 707.
Location/Qualifiers
1. 934
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4126706"
/tissue_type="neuroblastoma"
/lab_host="NIH_MGC_19"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 0.00404 Length: 934
Score: 86.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x BF311804 (1-934)

Qy 1 LeuValLeuLeuValLeuValLeuValTyrcysArgLysGluGly 18
|||||
Db 45 CTGGTCTGCTGCTGCTGCTCATCTCTGTTATTGCGGAGAGAGGGG 98

RESULT 4
BC033727

```

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/clone_lib="NIH_MGC_119"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:
Pred. No.:      0.00691      Length:      1532
Score:          86.00      Matches:      18
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              3          Gaps:      0

US-10-624-932C-2_COPY_372_389 (1-18) x BC033727 (1-1532)

QY      1      LeuValLeuLeuLeuValLeuLeuLeuValTyCysArgLysLysGluGly 18
Db      1266      CTGGTCCTGCTGCTGCTGCTCATCTCGTTATTGCGGAAGAAGGAGGG 1319

RESULT 5
CN691436
LOCUS
DEFINITION
Mus musculus E10.5 whole embryo cDNA library (Long) Mus
muscus cDNA clone NIA:E0309E05 IMAGE:30859828 5', mRNA sequence.
CN691436
ACCESSION
VERSION
KEYWORDS
SOURCE
Mus musculus
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 501)
Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
VanBuren,V., Falco,G., Martin,P.R., Staggs,C.A., Bassey,U.C.,
Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
Schlessinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A.,
Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
D'Urso,M., Kelsoe,J., Hide,W. and Ko,M.S.
Transcriptome analysis of mouse stem cells and early embryos
PLOS Biol. 1 (3), 410-419 (2003)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: E0309 row: E column: 05
Seq primer: M13 Reverse
High quality sequence stop: 501
POLYA=No.

FEATURES
source
1..501
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="nia:EST:E0309E05-5"
/db_xref="taxon:10090"
/clone="NIA:E0309E05 IMAGE:30859828"
/tissue_type="whole embryo including extraembryonic
tissues at 10.5-days postcoitum"
/dev_stage="E10.5"
/lab_host="DH10B"
/clone_lib="NIA Mouse E10.5 whole embryo cDNA library
(long)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: Salt;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]". Total
RNAs were extracted from a pool of 8 embryos at 10.5-days
postcoitum. Double-stranded cDNAs were synthesized with an

```


primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is ACGGACACG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:
Pred. No.: 0.00833 Length: 675
Score: 83.00 Matches: 15
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 96.51% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x CA315487 (1-675)

QY 1 LeuValLeuLeuValLeuValLeuValTyrCysArgLysGluGly 18
DB 350 CTCATCTTGCTGCTGCTGCTGCTGCTCATCTACTGCGCAGAGGAGGA 403

RESULT 8
BU613458
LOCUS
DEFINITION
UI-M-EWO-caz-d-10-0-UI.r1 NIH_BMAP_EWO Mus musculus cDNA clone
UI-M-EWO-caz-d-10-0-UI 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
JOURNAL
COMMENT

1 (bases 1 to 723)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

Location/Qualifiers
1. .723

FEATURES

source

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="UI-M-EWO-caz-d-10-0-UI"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_EWO"
/note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag

sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:
Pred. No.: 0.00897 Length: 723
Score: 83.00 Matches: 15
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 96.51% Indels: 0
DB: 5 Gaps: 0

US-10-624-932C-2_COPY_372_389 (1-18) x BU613458 (1-723)

QY 1 LeuValLeuLeuValLeuValLeuValTyrCysArgLysGluGly 18
DB 609 CTCATCTTGCTGCTGCTGCTGCTCATCTACTGCGCAGAGGAGGA 662

RESULT 9
BU612387

LOCUS
DEFINITION

UI-M-EWO-caz-j-06-0-UI.r1 NIH_BMAP_EWO Mus musculus cDNA clone

UI-M-EWO-caz-j-06-0-UI 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 756)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1. .756

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="UI-M-EWO-caz-j-06-0-UI"

/tissue_type="whole brain"

/dev_stage="embryo 15.5 dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH_BMAP_EWO"

/note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag

[illegible][illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:47:02 ; Search time 4321.67 Seconds
(without alignments)
1166.064 Million cell updates/sec

Title: US-10-624-932c-2_COPY_495_598

Perfect score: 559
Sequence: 1 TSNMTYGTFTNFGRLMIPN.....CCEPSPDSWLRLLKQSCG 104

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: gb.om.*
- 5: gb.ov.*
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- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	559	100.0	2688	9 BC009333	BC009333 Homo sapi
2	559	100.0	2697	6 AX451652	AX451652 Sequence
3	559	100.0	2752	6 AX449572	AX449572 Sequence
4	559	100.0	2881	6 AX527916	AX527916 Sequence

5	559	100.0	3580	6	AX367094	AX367094 Sequence
6	559	100.0	9700	6	AX054976	AX054976 Sequence
7	554	99.1	3844	10	BC058084	BC058084 Mus muscu
8	554	99.1	3992	10	MMU487852	AJ487852 Mus muscu
9	553	98.9	1787	6	BD057525	BD057525 Netrin re
10	553	98.9	2697	6	AX268596	AX268596 Sequence
11	553	98.9	2697	10	RNU87305	U87305 Rattus norv
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C 17	393.5	70.4	6522	6	BD186447	BD186447 Novel gen
18	393.5	70.4	121282	9	AC027318	AC027318 Homo sapi
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C 20	393.5	70.4	168168	2	AC012283	AC012283 Homo sapi
C 21	393.5	70.4	231407	2	AC139592	AC139592 Rattus no
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24	346	61.9	2962	5	AY187310	AY187310 Gallus ga
25	345	61.7	9328	10	AB118026	AB118026 Rattus no
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35	297	53.1	1438	6	AX054888	AX054888 Sequence
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ALIGNMENTS

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BC009333	IMAGE:4126760, partial cds.				
BC009333	GI:40226527				
BC009333	Homo sapiens (human)				
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Scheraga, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2688)
Strausberg, R.
Direct Submission
Submitted (12-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
On Dec 19, 2003 this sequence version replaced gi:11424611.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgrl.nih.gov
Ahter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granito, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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Db 473 ACAGGAATCAGCCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 532
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 533 TACCTCAGCTGCAACAGCGAAGACGTGAGGTTCCTCCCTAGCTGCTGTACACCCCTG 592
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 593 CTGAGTCCCATCGTGTAGCTGTGGACCCCTCGCTGCTCACCCTGAGTCTCATCTG 652
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
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Qy 101 SerCysGluGly 104
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AX451652 2697 bp DNA linear PAT 03-JUL-2002
LOCUS
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ACCESSION AX451652
VERSION AX451652.1 GI:21698587
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Koehler, R.H.
TITLE Regulation of human netrin binding membrane receptor unc5h-1
JOURNAL Patent: WO 0233080-A 1 25-APR-2002;
Bayer Aktiengesellschaft (DE)
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QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
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QY 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
DB 1663 CTGAGTCCCATGTTAGCTGTGGACCCCTGGCGTCTCTCACCGCGCCAGTCATCCTG 1722
QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGln 100
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QY 101 SerCysGluGly 104
DB 1783 TCGTGGAGGGC 1794

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LOCUS AX449572 2752 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1 from Patent WO0210216.
ACCESSION AX449572
VERSION AX449572.1 GI:21698195
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Padigaru,M., Mezes,P., Mishra,V., Burgess,C., Casman,S.,
Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Gerlach,V.L.,
Macdougall,J.R. and Smithson,G.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0210216-A 1 07-FEB-2002;
Curagen Corporation (US)
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QY 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
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QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGln 100
DB 1768 GCTATGGACCACTGTGGGGAGCCAGCCCTGCAGCTGAGGCTGCGCTCAAAAAGCAG 1827
QY 101 SerCysGluGly 104
DB 1828 TCGTGGAGGGC 1839

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LOCUS AX527916 2881 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 1 from Patent WO0229038.
ACCESSION AX527916
VERSION AX527916.1 GI:25172359
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Herrmann,J.L., Rastelli,L. and Shimkets,R.A.
TITLE Novel proteins and nucleic acids encoding same and antibodies
directed against these proteins
JOURNAL Patent: WO 0229038-A 1 11-APR-2002;
Curagen Corporation (US)
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DB 1749 CTGAGTCCCATGTTAGCTGTGGACCCCTGGCGTCTCTCACCGCGCCAGTCATCCTG 1808
QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGln 100
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ACCESSION AX367094
VERSION AX367094.1 GI:18855296
KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Griffin,J.A., Kallick,D.A., Triboulet,C.M., Yue,H., Nguyen,D.B.,
Tang,Y.T., Lai,P., Policky,J.L., Azimzai,Y., Lu,D.A., Graul,R.,
Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O.,
Patterson,C., Yang,J., Xu,Y., Warren,B.A., Ding,L. and
Sanjanwala,M.S.
Receptors
TITLE
JOURNAL
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Patent: WO 0198354-A 13 27-DEC-2001;
Incyte Genomics, Inc. (US)
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Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
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VERSION AX054976.1 GI:12228344
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Griffin,J.A., Kallick,D.A., Triboulet,C.M., Yue,H., Nguyen,D.B.,
Tang,Y.T., Lai,P., Policky,J.L., Azimzai,Y., Lu,D.A., Graul,R.,
Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O.,
Patterson,C., Yang,J., Xu,Y., Warren,B.A., Ding,L. and
Sanjanwala,M.S.
Receptors
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JOURNAL
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Query Match: 100.00% Indels: 0
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Qy 21 ThrGlyIleSerLeuLeuIleProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 158 ACAGGAATCAGCTCTCTATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 217
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 218 TACCTCAGCTGTCACACCGGAGACGTGAGTTGCCCTAGCTGGCTGTGACAGACCTG 277
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 278 CTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCTGCTCACCGGCCAGTCATCCTG 337
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 338 GCTATGGACCACTGTGGGAGCCCGCCCTGACAGCTGGAGCCTCGCCTCAAAAAGCAG 397
Qy 101 SerCysGluGly 104
Db 398 TCGTGGAGGCG 409

RESULT 7
BC058084
LOCUS BC058084 3844 bp mRNA linear ROD 21-OCT-2003
DEFINITION Mus musculus unc-5 homolog A (C. elegans), mRNA (cDNA clone
MGC:66671 IMAGE:16813463), complete cds.
ACCESSION BC058084
VERSION BC058084.1 GI:34784158
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heien,F.,
Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
```

Fahey, J., Helton, E., Ketterman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.C., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E., Scherch, A., Schein, D.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257
12477932
2 (bases 1 to 3844)
Strausberg, R.
Direct Submission
Submitted (08-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Teai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 126 Row: b Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23346570.

FEATURES

source

Location/Qualifiers
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/note="Vector: pYX-ASC"
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QLSNGHLLSPGSGRHTLHSSPTSEASDFVRLSTQNYFRSLPRGTSNAYGTNFLL
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gene

CDS

GVLLTRPVILAMDHCGEPPDSWSLRLLKKQCEGSWEDVLHLEESPSHLYYCOLEAG
ACYVTEQLGRFALVGEALSVAATKRLRLLLFPVACTSLEYNIYVLCIHDTHDLKE
VVOLEQLGGQLIQPRVLVHFADS VHNRLSLTHDVPSSLWKSILVSVQEI PFYHWN
GTQOVLHCTFTLERVNASTDOLACKVWVQVEGDSQSNINENITKDRPAMLALES
EGGVPLVGPASAFKIPFLIRQKIITSLDPPGSRGADWRLTAKLHLDHLSLFSFASKPS
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714..926
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/note="TSP1; Region: Thrombospondin type 1 repeats"
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1566..1877
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netrin receptors"
/db_xref="CDD:smart00218"
2496..2684
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/note="DEATH; Region: DEATH domain, found in proteins
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present in a variety of proteins with apoptotic functions.
Some (but not all) of these domains form homotypic and
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ORIGIN

Alignment Scores:

Pred. No.:	1.766-47	Length:	3844
Score:	554.00	Matches:	103
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Best Local Similarity:	99.04%	Mismatches:	1
Query Match:	99.11%	Indels:	0
DB:	10	Gaps:	0

US-10-624-932C-2_COPY_495_598 (1-104) x BC058084 (1-3844)

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QY	41	TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCyGlnThrLeu	60
DB	1686	TACCTCACTCTGCACAGCAGACGTGAGGTTCGCCCTAGCTGGCTGTACAGACCTGT	1745
QY	61	LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu	80
DB	1746	CTGAGTCTCTATCGTTAGCTGTGGGCCCCCAGAGGTCTGCTACCCGCCAGTCACTCT	1805
QY	81	AlaMetAepHisCysGlyGluProSerProAepSerTrpSerLeuArgLeuLysGln	100
DB	1806	GCCATGGACCACTGGGGGAGCCCCAGTCCCCGACAGCTGGAGCCTGGGCTCAAAAAGCAG	1865
QY	101	SerCysGluGly 104	
DB	1866	TCCTGTGAGGCG 1877	

RESULT 8

MMU487852	MMU487852	3992 bp	mRNA	linear	ROD 24-SEP-2002
LOCUS	Mus musculus mRNA for netrin receptor Unc5h1 (Unc5h1 gene).				
DEFINITION					
ACCESSION	AJ487852				
VERSION	AJ487852.1	GI:22035783			
KEYWORDS	netrin receptor Unc5h1; Unc5h1 gene.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Engelkamp,D.
Cloning of three mouse Unc5 genes and their expression patterns at mid-gestation
Mech. Dev. 118 (1-2), 191-197 (2002)
22319710
PUBMED 12351186
2 (bases 1 to 3992)
Engelkamp,D.
Direct Submission
TITLE Direct Submission
JOURNAL Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for Brain Research, Deutscherordenstrasse 46, Frankfurt 60528, GERMANY
Location/Qualifiers
1..3992 /organism="Mus musculus"
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SLEQIVLPKPPGIPAEVEMLRNEDLPDLPNVIYTRHSLVVRQAARLADTAN
YTCVAKNIVARRRASAIVIVYVNGHSTWTEWVCSASCGRGQKRSRCTNPAPLN
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RGADLTNRCTSDLCHTSSGPDVALYIGLVAVALILLVLLVLYICRKGGLDS
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RLMIPNTGISILLIPDAPCKIYEIVLTLLKPEDVRLPLAGCOTLLSPIVSCGPGV
LLTRPVLAMHDCGSPDSSNLRKKQSCGSEWEDVHLGSESPSHLYICQLBAGAC
YLEFQUGRFLAVGEALSVAAKRLRLLLFPAPVACTSLEYNIRVYLHLDHDAKEV
QLEKQLGQLIQEPRVLFKDSYHNLRLSHDVPSSKLLYSYQEIPEYHWTG
QOYLCTPLTRVNASDIAKVVWQVEGDGQSFNINFTKDTFPAEMLAISEG
GVPAIVGPSAFKIPFLRQKITSLDPPCSRGAWRTLAOKLHDLHLSFPSPKPSPT
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ORIGIN
Alignment Scores:
Pred. No.: 1.83e-47 Length: 3992
Score: 554.00 Matches: 103
Percent Similarity: 99.04% Conservative: 0
Best Local Similarity: 99.04% Mismatches: 1
Query Match: 99.11% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x MMU487852 (1-3992)
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Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1774 ACAGGAATGCGCTCTCATACCCCGAGCGCCATCCCGAGGAGAAATCTACGAGATC 1833
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1834 TACCTCACTCTGCACAGCCAGACGCTGAGGTTGCCCTAGCTGGCTGTGACAGCCCTG 1893
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1894 CTGAGTCTCATCTGTTAGCTGTGGGCCCCCAGAGTCTCTGCTACCCGCCAGTATCTTT 1953
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100

REFERENCE 1
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE 2
AUTHORS
TITLE
JOURNAL
FEATURES
source
gene
CDS

1054 GCCATGACCACTCGCGGGAGCCCGAGTCCCGACAGCTGGAGCTCGGCTCAAAAAGCAG 2013
101 SerCysGluGly 104
2014 TCCTGTGAGGCG 2025
RESULT 9
BD057525
LOCUS
DEFINITION Netrin receptors.
ACCESSION BD057525
VERSION BD057525.1 GI:22603131
KEYWORDS JP 2001505062-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1787)
AUTHORS Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.
TITLE Netrin receptors
JOURNAL Patent: JP 2001505062-A 2 17-APR-2001;
THE REGENTS OF THE UNIV OF CALIFORNIA
COMMENT PN JP 2001505062-A/2
PD 17-APR-2001
PF 19-FEB-1998 JP 1998536840
PR 19-FEB-1997 US 08/808982
PI MARC TESSIER LAVIGNE,DAVID & LEONARDO,LINDSAY HINCK,MASAYUKI
PI MASU,
PI KAZUKO KEINO MASU
PC C07K1/00,C07K14/00,C07H21/02,C07H21/04,G01N33/53 CC
Strandedness: Double;
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FH Key Location/Qualifiers.
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Score: 553.00 Matches: 103
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Query Match: 98.93% Indels: 0
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Db 519 ACAGGAATGCGCTCTCATACCCCGAGCGCCATCCCGAGGAGAAATCTATGAGATC 578
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 579 TACCTCACTCTGCACAGCCAGACGCTGAGGTTGCCCTAGCTGGCTGTGACAGCCCTG 638
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
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Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 699 GCTATGACCACTCTGTGGGGAGCCCGAGCTGACAGCTGGAGCTGGCCCTCAAAAAGCAG 758
Qy 101 SerCysGluGly 104
Db 759 TCCTGTGAGGCGA 770

RESULT 10
 LOCUS AX268596 2697 bp DNA linear PAT 29-OCT-2001
 DEFINITION Sequence 15 from Patent WO0175440.
 ACCESSION AX268596
 VERSION AX268596.1 GI:16541710
 KEYWORDS
 SOURCE Rattus sp.
 ORGANISM Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1
 AUTHORS Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and Pratt,J.Y.

TITLE Schizophrenia related genes
 JOURNAL Patent: WO 0175440-A 15 11-OCT-2001;
 WELFIDE CORPORATION (JP)

FEATURES
 source Location/Qualifiers
 1..2697

/organism="Rattus sp."
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/db_xref="taxon:10118"

ORIGIN

Alignment Scores:
 Pred. No.: 1,54e-47 Length: 2697
 Score: 553.00 Matches: 102
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 Query Match: 98.93% Indels: 0
 DB: 6 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x AX268596 (1-2697)

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Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
 Db 1603 TACCTCACATGCACAGCCAGAGAGCTGAGTTGCCCTAGCTGGCTGTGACAGCCCTG 1662

Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
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Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuIleGln 100
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Qy 101 SerCysGluGly 104

Db 1783 TCCTCGAGGGC 1794

RESULT 11

LOCUS RNU87305 2697 bp mRNA linear ROD 15-MAY-1997
 DEFINITION Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds.
 ACCESSION U87305
 VERSION U87305.1 GI:2055391

KEYWORDS
 SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 2697)

AUTHORS

Leonardo,B.D., Hinck,L., Masu,M., Keino-Masu,K., Ackerman,S.L. and Tessier-Lavigne,M.

Vertebrate homologues of C. elegans UNC-5 are candidate netrin

JOURNAL Nature 386 (6627), 833-838 (1997)
 MEDLINE 97271897
 PUBMED 9126742

REFERENCE

2 (bases 1 to 2697)
 Leonardo,B.D., Hinck,L., Masu,M., Keino-Masu,K. and Tessier-Lavigne,M.

Direct Submission

Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus, San Francisco, CA 94143-0452, USA

FEATURES

source

Location/Qualifiers

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YTCVAKNIVARRISAAVYVYNGWSTWTEWSCASCGRWQKRSCNTNPAPLN
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DVADSSILTSGFQPVSIKPSKADNPILLITIQDLSLTITTTTQGSICSDQDGPSPKFLG
SNGLHSLPLSGRHTLHSSPTSEADPVSRLSTONYFRSLPRGTSMAYGTFFNLGG
RLMPTNGISILLIPDAIPRCKIYEIVLTILKPEDVRLPLAGCOTLLSPVYSCGPGV
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LYFTQEGRFALVGEALSVAATLRLLFPACTSLEYINIRVYLDHDTHDALKEVV
QLEKQAGLQITQEPVLFKDSYHNLRSLSDHVPSSLWKSLLYSYQIRIPFYHWNGT
QOYLKQFTFLERINASTDLACKVWVMOVEDGGSFNFINITKTOTRAEALLAISEG
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AMILNLWEARHPFNGNLQGLAAAVAGLGPDAGLFTVSEASC"

ORIGIN

Alignment Scores:

Pred. No.: 1,54e-47 Length: 2697
 Score: 553.00 Matches: 102
 Percent Similarity: 99.04% Conservative: 1
 Best Local Similarity: 98.08% Mismatches: 1
 Query Match: 98.93% Indels: 0
 DB: 10 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x RNU87305 (1-2697)

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Db 1483 ACCAGCAACATGGCCTACGGGACCTTCAACTTCTCGGGGGCGGCTGATGATCCCTAAT 1542

Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyIleTyrGluIle 40

Db 1543 ACGGGGATCAGCCTCTCATACCCCGGATGCCATCCCGGAGGAAGATCTACAGAGATC 1602

Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60

Db 1603 TACCTCACATGCACAGCCAGAGAGCTGAGTTGCCCTAGCTGGCTGTGACAGCCCTG 1662

Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80

Db 1663 CTGAGTCCAGTCTTAGCTGTGGGCCCCCAGGAGTCTCTGCTCACC CGCCAGTCATCCTT 1722

Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuIleGln 100

Db 1723 GCAATGGACCACTGTGGAGAGCCAGCCCTGACAGCTGAGTCTCGGCTCAAAAAGCAG 1782

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Qy 101 SerCysGluGly 104
|||||
Db 1783 TCCTGCGAGGGC 1794

RESULT 12
BD057524
LOCUS BD057524 3014 bp DNA linear PAT 27-AUG-2002
DEFINITION Netrin receptors.
ACCESSION BD057524
VERSION BD057524.1 GI:22603130
KEYWORDS JP 2001505062-A/1.
SOURCE synthetic construct
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 3014)
AUTHORS Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.
TITLE Netrin receptors
JOURNAL Patent: JP 2001505062-A 1 17-APR-2001;
THE REGENTS OF THE UNIV OF CALIFORNIA
COMMENT PN JP 2001505062-A/1
PD 17-APR-2001
PR 19-FEB-1998 JP 1998536840
PF 19-FEB-1997 US 08/808982
PI MARC TESSIER LAVIGNE,DAVID E LEONARDO,LINDSAY HINCK,MASAYUKI
PI MASU.
PI KAZUKO KEINO MASU
PC C07K1/00,C07K14/00,C07K17/00,C07H21/02,C07H21/04,G01N33/53 CC
Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.
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source 1..3014
/mol_type="synthetic construct"
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ORIGIN
Alignment Scores:
Pred. No.: 1.73e-47 Length: 3014
Score: 553.00 Matches: 102
Percent Similarity: 99.04% Conservative: 1
Best Local Similarity: 98.08% Mismatches: 1
Query Match: 98.93% Indels: 0
DB: 6 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x BD057524 (1-3014)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
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Db 1483 ACCAGCAACATGGCTACGGACNCTTCAACTTCCTCGGGGCGGGTGATGATCCCTAAT 1542
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
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Db 1543 ACGGGGATCAGCTCTCATACCCCGGATGCCATCCCGGAGGAAAGATCTACGAGATC 1602
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
|||||
Db 1603 TACTTCACATGCAACAGCCAGAGACGTGAGGTTCCTCGGGCTGTGACAGCCCTG 1662
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
|||||
Db 1663 CTGAGTCAGTCGTAGCTGTGGGCCCCCAGGAGTCTCTGCTCACCGGCCAGTCATCCTT 1722
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
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Db 1723 GCAATGGACCACTGTGGAGAGCCAGCCCTGACAGCTGAGTCTCGGCTCAAAAAGCAG 1782
Qy 101 SerCysGluGly 104
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Db 1783 TCCTGCGAGGGC 1794

RESULT 13
AX054892
LOCUS AX054892 813 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 7 from Patent WO0073328.
ACCESSION AX054892
VERSION AX054892.1 GI:12228303
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS van Criekeinge,W., Roelens,I., Bogaert,T. and Verwaerde,P.
TITLE Unc-5 constructs and screening methods
JOURNAL Patent: WO 0073328-A 7 07-DEC-2000;
Devgen NV (BE)
FEATURES
Location/Qualifiers
source 1..813
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
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Pred. No.: 1.19e-44 Length: 813
Score: 520.00 Matches: 104
Percent Similarity: 97.20% Conservative: 0
Best Local Similarity: 97.20% Mismatches: 0
Query Match: 93.02% Indels: 3
DB: 6 Gaps: 0
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Db 449 ACCAGCAACATGGCTACGTATGGACCTTCAACTTCCTCGGGGCGGGTGATGATCCCTAAT 508
Qy 21 ThrGlyIle-SerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
|||||
Db 509 ACAGGATCAAGCTCTCTATCCCGCCAGATGCCATACCCGAGGGAAGATCTATGAGAT 568
Qy 40 eTyrLeuThr-LeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrL 60
|||||
Db 569 CTACCTCAGCTTGCACAAGCCGGAAGACGTGAGGTTCGCCCTAGCTGGCTGTGAGACCC 628
Qy 60 euleuSerProIleValSer-CysGlyProProGlyValLeuLeuThrArgProValIle 79
|||||
Db 629 TGCTGATTCATCGTTAGCTTGGACCCCTCGCGCTCTGCTCACCGGCCAGTCATC 688
Qy 80 LeuAlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLys 99
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Db 689 CTGCTATGGACCACTGTGGGAGCCCGCCAGCTGACAGCTGGAGCTCGGCTCAAAAAG 748
Qy 100 GlnSerCysGluGly 104
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Db 749 CAGTCGTGCGAGGGC 763
RESULT 14
CQ730306
LOCUS CQ730306 2784 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 16240 from Patent WO02068579.
ACCESSION CQ730306
VERSION CQ730306.1 GI:42303801
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 16240 06-SEP-2002;
PE Corporation (NY) (US)
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Location/Qualifiers
1. .2784
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ORIGIN

Alignment Scores:

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Query Match: 83.27% Indels: 15
DB: 6 Gaps: 1

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Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyGluIle 40
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Qy 41 TyrLeuThrLeuHisLysProGluHspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
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Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
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Db 1762 -----GTGAGCTGTGGAGCCCTCGCTGCTCACCAGCGGCGAGTCATCCTG 1809
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Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTroSerLeuArgLeuLysGln 100
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Qy 101 SerCysGluGly 104
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Db 1870 TCGTGGAGGCG 1881
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RESULT 15

AC123700/c

LOCUS

AC123700 242128 bp DNA linear HTG 09-MAR-2004
Mus musculus chromosome 13 clone RP23-335A11 map 13, *** SEQUENCING
IN PROGRESS ***, 7 unordered pieces.

ACCESSION

AC123700.4 GI:45268905

HTG; HTGS_PHASE1; HTGS_FULPTOP; HTGS_ACTIVEFIN.

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 242128)

Mus musculus chromosome 13, clone RP23-335A11

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,I.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Collangelo,M., Collins,S., Collumore,A.,
Cook,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Paro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazaras,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrum,J.,
Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,
Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,

TITLE

JOURNAL

REFERENCE

AUTHORS

Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 242128)
Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collumore,A., Cook,A., Cooke,P., Corum,B., DeArrellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,X., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrum,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL

COMMENT

Submitted (09-MAR-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 9, 2004 this sequence version replaced gi:28933837.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WTHR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L26431
Center clone name: 335_A_11

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 80291: contig of 80291 bp in length
* 80292 80391: gap of 100 bp
* 80392 105410: contig of 25019 bp in length
* 105411 105510: gap of 100 bp
* 105511 173922: contig of 67412 bp in length
* 173923 173922: gap of 100 bp
* 173923 182093: contig of 9071 bp in length
* 182094 182193: gap of 100 bp
* 182194 207358: contig of 25165 bp in length
* 207359 207458: gap of 100 bp
* 207459 222746: contig of 15288 bp in length
* 222747 222846: gap of 100 bp
* 222847 242128: contig of 19282 bp in length.

FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

/chromosome="13"
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/clone="RP23-335A11"
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ORIGIN

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Percent Similarity: 47.46% Conservative: 0
Best Local Similarity: 47.46% Mismatches: 0
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DB: 2 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x AC123700 (1-242128)

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Qy	41	TyrLeuThrLeuHisLysProGluaspVal	50
Db	145348	TACCTCACTCTGCACAGCCAGAGACGTGAGGTGTGTGCCCTGCTGTGTGTGTGG	145289
Qy	50	-----	50
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Qy	50	-----	50
Db	145228	AGCACTGCTGTACCTGTTCTGACCTGGCCCGAGGAGCACAGGGGATGAGGCGCACTTAA	145169
Qy	50	-----	50
Db	145168	GCTCACCCCTGATTGCAACTTCCGTCTTACGGTGTCAACCCCACTGCAGAGTCTGT	145109
Qy	50	-----	50
Db	145108	CTCCTAACCCCAACGGTCTCTAGGACTGGCCACTGACGGCTTTCCTCTCCACCATGTTT	145049
Qy	51	-----ArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleValSerCys	67
Db	145048	CCCCACTTGAGGTGGCCCTAGCTGGCTGTGAGACCCCTGTGAGTCTCTATCGTTAGCTGT	144989
Qy	68	GlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCysGlyGlu	87
Db	144988	GGGCCCCCAGGAGTCTGCTCACCGGCCAGTCATCTTGCATGGACCACTGCGGGGAG	144929
Qy	88	ProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGly	104
Db	144928	CCCAGTCCCGACAGCTGGAGCTGGGCTCAAAAAGCAGTCTCTGTGAGGGC	144878

Search completed: September 9, 2005, 09:42:25
Job time : 4362.67 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 20:54:46; Search time 537.856 Seconds
(without alignments)
1144.643 Million cell updates/sec

Title: US-10-624-932C-2_COPY_495_598

Perfect score: 559

Sequence: 1 TSNMTYGTFTFLGRLMIEN.....CGEPPDSWSLRLKKQSCGE 104

Scoring table:

BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	559	100.0	2463	12	Adh71623 Human gen
2	559	100.0	2575	12	Adh71621 Human gen
3	559	100.0	2635	11	Adn95100 Human LEC
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5	559	100.0	2752	6	Abk37922 cDNA enco

6	559	100.0	2752	12	ADH71617	Adh71617 Human gen
7	559	100.0	2881	6	ABK49422	Abk49422 DNA enco
8	559	100.0	2881	10	ADG42568	Adg42568 Novel hum
9	559	100.0	2881	12	ADH71649	Adh71649 Human gen
10	559	100.0	2881	12	ADH71635	Adh71635 Human gen
11	559	100.0	2881	12	ADH71637	Adh71637 Human gen
12	559	100.0	2881	12	ADH71641	Adh71641 Human gen
13	559	100.0	2881	12	ADH71609	Adh71609 Human gen
14	559	100.0	2881	12	ADH71629	Adh71629 Human gen
15	559	100.0	2881	12	ADH71645	Adh71645 Human gen
16	559	100.0	2881	12	ADH71627	Adh71627 Human gen
17	559	100.0	2881	12	ADH71639	Adh71639 Human gen
18	559	100.0	2881	12	ADH71643	Adh71643 Human gen
19	559	100.0	2881	12	ADH71625	Adh71625 Human gen
20	559	100.0	2881	12	ADH71647	Adh71647 Human gen
21	559	100.0	3561	12	ADL06497	Adl06497 Human tum
22	559	100.0	3580	6	ABK15169	Abk15169 Human RSP
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24	555	99.3	2881	12	ADH71631	Adh71631 Human gen
25	554	99.1	2880	12	ADH71633	Adh71633 Human gen
26	553	98.9	1787	2	AAV52941	Aav52941 Human UNC
27	553	98.9	2697	6	AAS16843	Aas16843 Rat netri
28	553	98.9	3014	2	AAV52940	Aav52940 Rat UNC-5
29	520	93.0	813	4	AAC90917	Aac90917 Human pro
30	503	90.0	1321	4	AAH99530	Aah99530 Human pro
31	465.5	83.3	2907	4	AAK52261	Aak52261 Human pol
32	393.5	70.4	6522	8	AAI51204	Aai51204 Human gen
33	393.5	70.4	9582	4	AAD16560	Aad16560 Human nov
34	393.5	70.4	9582	6	ABS64150	Abs64150 Human apo
35	393.5	70.4	9582	10	AAD60459	Aad60459 Human sec
36	393.5	70.4	18772	4	AAD16561	Aad16561 Human nov
37	393.5	70.4	18772	6	ABS64151	Abs64151 Human apo
38	393.5	70.4	18772	10	AAD60460	Aad60460 Human sec
39	374	66.9	604	6	ABK52893	Abk52893 Human net
40	337	60.3	2786	10	AAI56266	Aai56266 Human thr
41	337	60.3	2986	13	ADR95249	Adr95249 Human lro
42	337	60.3	3646	5	AAS75738	Aas75738 DNA enco
43	337	60.3	3646	13	ADR99257	Adr99257 Human unc
44	333	59.6	1575	4	AAC90916	Aac90916 Human UNC
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ALIGNMENTS

RESULT 1
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ID ADH71623 standard; DNA; 2463 BP.
XX
AC ADH71623;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21h SEQ ID NO:519.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.

ADH71621
ID ADH71621 standard; DNA; 2575 BP.
XX
AC ADH71621;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21g SEQ ID NO:517.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PW WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PP 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0387969P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
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PR 12-JUN-2002; 2002US-0388022P.
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PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389723P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Caterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VV, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
PI Zhong H;
XX
WPI: 2004-081935/08.
P-PSDB; ADH71622.
XX
DR New NOVX polypeptides and nucleic acid molecules useful for preventing or
XX treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
PT
XX
XX
PS Example 21; SEQ ID NO 517; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaeamic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
XX encodes a NOVX polypeptide of the invention.
SQ Sequence 2575 BP; 490 A; 873 C; 754 G; 458 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,54e-53 Length: 2575
Score: 559.00 Matches: 104
Percent Similarity: - 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

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US-10-624-932C-2_COPY_495_598 (1-104) x ADH71621 (1-2575)
Qy 1 ThrSerAenMetThrTyrGlyThrPheAenPheLeuGlyArgLeuMetIleProAen 20
Db 1290 ACCAGCAACATGACCTATGGACCTTCAACTTCCTCGGGGGCGGCTGATCCCTAAT 1349
Qy 21 ThrGlyIleSerLeuLeuIleProProAenPheLeuGlyArgLeuMetIleProAen 40
Db 1350 ACAGGAATCAGCTTCCTATCCCTCCAGATGCCATACCCAGGAGAGATCTATGAGATC 1409
Qy 41 TyrLeuThrLeuHisLeuValProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1410 TACCTCAGCTGCGACAGCCGAGAGAGCTGAGTGGCTGCCCTAGCTGCTGCACACCTG 1469
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1470 CTGAGTCCCATCGTTAGCTGTGGACCCCTGGCTGCTGCTCACCCGCGCAGTCACTCTG 1529
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuIleValGln 100
Db 1530 GCTATGGACCACTGTGGGAGCCAGCCCTGCACAGCTGGAGCCTGGCCCTCAAAAGCAG 1589
Qy 101 SerCysGluGly 104
Db 1590 TCGTGGAGGGC 1601
RESULT 3
ID ADN95100
XX ADN95100 standard; DNA; 2635 BP.
XX AC ADN95100;
XX DT 01-JUL-2004 (first entry)
XX DE Human LEC gene sequence SeqID22.
XX KW growth; differentiation; blood endothelial cell; BEC;
XX KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
XX KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
XX KW vasotrophic; antiinflammatory; gene therapy; endothelial cell disorder;
XX KW inflammatory disease; cancer metastasis; lymphatic system; gene; ds;
XX KW human.
XX OS Homo sapiens.
XX PN WO2003080640-A1.
XX PD 02-OCT-2003.
XX PF 07-MAR-2003; 2003WO-US006900.
XX PR 07-MAR-2002; 2002US-0363019P.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (LICN) LICENTIA LTD.
XX PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
XX DR WPI; 2003-876899/81.
XX DR P-PSDB; ADN95115.
XX PS Claim 23; SEQ ID NO 22; 176pp; English.
XX CC This invention relates to a method of differentially modulating the
CC growth or differentiation of blood endothelial cells (BEC) or lymphatic
CC endothelial cells (LEC) comprises contacting endothelial cells with a
CC composition comprising an agent that differentially modulates blood or
CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises
CC identifying a human subject with lymphoedema and with a mutation in at
CC least one allele of a gene encoding a LEC protein, where the mutation
CC correlates with lymphoedema in human subjects, and with the proviso that
CC the LEC protein is not VEGFR-3; and administering to the subject a
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composition comprising a lymphatic growth agent selected from VEGF-C or
VEGF-D polypeptides and polynucleotides. The invention may be useful for
the development of compounds with an antiangiogenic, cytostatic,
vasotrophic or antiinflammatory activity or for gene therapy. The method
is useful in modulating the growth or differentiation of blood
endothelial cells or lymphatic endothelial cells, in treating hereditary
lymphoedema, in screening for an endothelial cell disorder or
predisposition to the disorder or in monitoring the efficacy or toxicity
of a drug on endothelial cells. The agent is useful in manufacturing a
medicament for the differential modulation of blood vessel endothelial
cell or lymphatic vessel endothelial cell growth or differentiation. The
lymphatic growth agent may also be used in manufacturing a medicament for
the treatment of hereditary lymphoedema resulting from a mutation in a
LEC gene or of other diseases involving the lymphatic vessels, such as
various inflammatory diseases and cancer metastasis via the lymphatic
system. The present sequence is that of a human LEC/BEC differentially
expressed gene which is related to the method of the invention. Note: The
sequence data for this patent did not form part of the printed
specification but was obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pat_sequences
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Sequence 2635 BP; 483 A; 935 C; 722 G; 495 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.71e-53 Length: 2635
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x ADN95100 (1-2635)

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Qy 1 ThrSerAenMetThrTyrGlyThrPheAenPheLeuGlyArgLeuMetIleProAen 20
Db 413 ACCAGCAACATGACCTATGGACCTTCAACTTCCTCGGGGGCGGCTGATCCCTAAT 472
Qy 21 ThrGlyIleSerLeuLeuIleProProAenPheLeuGlyArgLeuMetIleProAen 40
Db 473 ACAGGAATCAGCTTCCTATCCCTCCAGATGCCATACCCAGGAGAGATCTATGAGATC 532
Qy 41 TyrLeuThrLeuHisLeuValProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 533 TACCTCAGCTGCGACAGCCGAGAGAGCTGAGGTTGCCCTAGCTGCTGCACACCTG 592
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 593 CTGAGTCCCATCGTTAGCTGTGGACCCCTGGCTGCTCCTCACCCGCGCAGTCACTCTG 652
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuIleValGln 100
Db 653 GCTATGGACCACTGTGGGAGCCAGCCCTGCACAGCTGGAGCCTGGCCCTCAAAAGCAG 712
Qy 101 SerCysGluGly 104
Db 713 TCGTGGAGGGC 724
```

RESULT 4
ABK52891
ID ABK52891 standard; DNA; 2697 BP.

XX AC ABK52891;

XX DT 27-AUG-2002 (first entry)

XX DE Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.

XX KW Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human;

XX KW neurotrophic; neuroprotective; cytostatic; antiparkinsonian;

XX KW cerebroprotective; cancer; central nervous system; CNS; stroke;

XX KW Parkinson's disease; multiple sclerosis; Alzheimer's disease.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT CDS 1..2697
FT /tag= a
FT /product= "Netrin binding membrane receptor UNC5H-1"
XX PN WO200233080-A2.
XX PD 25-APR-2002.
XX PF 15-OCT-2001; 2001WO-EP011891.
XX PR 16-OCT-2000; 2000US-0240061P.
XX PA (FARB) BAYER AG.
XX PI Koehler RH;
XX DR WPI; 2002-463314/49.
XX DR P-PSDB; AAU97899.
XX PT Novel human netrin binding membrane receptor polypeptide and
PT polynucleotides for identifying modulating agents useful in treating
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
PT Alzheimer's disease.
XX PS Claim 1; Fig 1; 94pp; English.
XX CC This invention relates to the DNA and protein sequences of a novel
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC acid encoding the invention is useful as a probe for detecting a nucleic
CC of the invention are useful to screen for agents which decrease the
CC activity of the UNC5H-1 protein. The sequences are also useful for
CC screening agents which regulate (modulate) the activity of the protein of
CC the invention. A pharmaceutical composition containing the protein of the
CC invention or a reagent that modulates the activity of the UNC5H-1 protein
CC may be useful for treating a UNC5H-1 dysfunction related disease such as
CC cancer or a central nervous system (CNS) disorders (e.g. Parkinson's
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
CC proteins comprising the UNC5H-1 protein are useful for generating
CC antibodies and for in various assay systems, and the protein can be used
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
CC of the invention is useful for detecting a coding sequence for the UNC5H-
CC 1 protein. The present sequence represents a DNA sequence encoding the
CC human netrin binding membrane receptor UNC5H-1 protein of the invention
XX SQ Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5,886-53 Length: 2697
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x ABK52891 (1-2697)

QY 1 ThrSerAnMetThrTyrGlyThrPheAnPheLeuGlyGlyArgLeuMetIleProAn 20
DB 1483 ACCAGCAACATGACCTATGGGACCTTCACTTCCTCGGGGGCGGCTGATGATCCCTAAT 1542
QY 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
DB 1543 ACAGGAAATCAGCTCTCTATCCCCCAGATGTCATACCCGAGGGAAGATCTATGAGATC 1602
QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
DB 1603 TACCTCAGCTGCACAAGCCGAGACGTCGTAGGTTGCCCTAGCTGGCTGTCAGACCCCTG 1662
QY 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80

Db 1663 CTGAGTCCCATCGTTAGCTGTGGAGCCGCCCTGGCGTCTGCTCACCCGGCCAGTCAATCCTG 1722
QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1723 GCTATGGACCACTGTGGGAGCCGCCAGCTGACAGCTGGAGCTGCGCTCAAAAAGCAG 1782
QY 101 SerCysGluGly 104
Db 1783 TCGTGCAGGGC 1794
RESULT 5
ABK37922
ID ABK37922 standard; cDNA; 2752 BP.
XX AC ABK37922;
XX DT 21-MAY-2002 (first entry)
XX DE cDNA encoding Human protein NOV1.
XX KW Human; NOVX; ss; gene; cardiomyopathy; atherosclerosis; diabetes;
KW cell signal processing disorder; metabolic disorder; obesity; infection;
KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
KW psychosis; neurological disorder; anxiety; schizophrenia;
KW manic depression; dementia; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome; gene therapy.
XX OS Homo sapiens.
XX PN WO200210216-A2.
XX PD 07-FEB-2002.
XX PF 30-JUL-2001; 2001WO-US024225.
XX PR 28-JUL-2000; 2000US-0221409P.
PR 04-AUG-2000; 2000US-0222840P.
PR 04-AUG-2000; 2000US-0223752P.
PR 04-AUG-2000; 2000US-0223762P.
PR 04-AUG-2000; 2000US-0223769P.
PR 14-AUG-2000; 2000US-0223770P.
PR 15-AUG-2000; 2000US-0225146P.
PR 15-AUG-2000; 2000US-0225392P.
PR 15-AUG-2000; 2000US-0225470P.
PR 16-AUG-2000; 2000US-0225697P.
PR 01-FEB-2001; 2001US-0263662P.
PR 05-APR-2001; 2001US-0281645P.
XX (CURA-) CURAGEN CORP.
XX PI Padigaru M, Mezes P, Mishra V, Burgess C, Casman S, Groese WM;
PI Alsbrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;
XX WPI; 2002-180074/23.
XX DR P-PSDB; AAU85403.
XX PT New isolated cytoplasmic, nuclear, membrane bound, or secreted
PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
PT immune disorders.
XX PS Claim 9; Page 9-10; 213pp; English.
XX CC The invention relates to an isolated cytoplasmic, nuclear, membrane
CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
CC form. Also included are the nucleic acids encoding the NOVX proteins, a
CC vector comprising the nucleic acid, a cell comprising the vector, an anti
CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
CC antibody are useful for treating or preventing a NOVX-associated

CC disorder, where the disorder is selected from cardiomyopathy,
CC atherosclerosis, diabetes, a disorder related to cell signal processing
CC and metabolic pathway modulation, metabolic disorders, obesity,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases, bacterial, fungal, protozoal and viral infections, pain,
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC hypertrophy, and psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC nucleic acid is useful in gene therapy. The present sequence encodes a
CC NOVX protein
XX
SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.04e-53 Length: 2752
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x ABK37922 (1-2752)

QY 1 ThrSerAenMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
DB 1528 ACCAGCAACATGACCTATGGGACCTTCACTTCCTGGGGGGCCGGCTGATGATCCCTAAT 1587
QY 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
DB 1588 ACAGGTATCAGCCTCTCATCCCCCAGATGCCATACCCGAGGAGAGATCTATGAGATC 1647
QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrIleu 60
DB 1648 TACTTCAGCTGCAACACCGGAGACGTGAGGTGGCCCTAGCTGGCTGTGCAGACCCCTG 1707
QY 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
DB 1708 CTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCTGCTACCCGGCCAGTCATCTCTG 1767
QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
DB 1768 GCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCCTCGGCTCAAAAAGCAG 1827
QY 101 SerCysGluGly 104
DB 1828 TCGTGGAGGGC 1839

RESULT 6
ADH71617
ID ADH71617 standard; DNA; 2752 BP.
XX AC ADH71617;
XX DT 25-MAR-2004 (first entry)
XX DE Human gene of the invention NOV21e SEQ ID NO:513.
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; anticipaeic; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX OS Homo sapiens.
XX PN WO2003102155-A2.

XX 11-DEC-2003.
PD 03-JUN-2003; 2003WO-US017430.
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 07-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-038796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 08-JUN-2002; 2002US-0387262P.
PR 10-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 11-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 12-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389894P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-040617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.

PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Alvarez E, Anderson DM, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gargolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JU, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenburg ME, Sciore P, Shenoy SG, Shinkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX WPI: 2004-081935/08.
DR P-PSDB; ADH71618.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 513; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX) . A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.04e-53 Length: 2752
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x ADH71617 (1-2752)

QY 1 ThrSerAsnMetThrTyrglyThrPheAsnPhLeuGlyArgLeuMetileProhen 20
DB 1528 ACCAGCAACATGACCTATGGGACCTTCACTTCTCGGGGGCGGCTGATGATCCCTAAT 1587
QY 21 ThrGlyIleSerLeuLeuileProProAspAlaileProArgGlyLysileTyrglulle 40
DB 1588 ACAGGTATCAGCTCTCTATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 1647
QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
DB 1648 TACCTCAGCTGCACAAAGCGGAAGAGCTGAGGTGGCTTGCCTAGCTGCTCAGACCTG 1707
QY 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
DB 1708 CTGAGTCCCATCGTTAGCTGTGGACCCCTCGTGGCGTCTCTCACCAGCGGCAGTCATCCTG 1767

QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGln 100
DB 1768 GCTATGGACCACTGTGGGAGCCAGCCCTGACAGCTGGAGCTGGCCCTCAAAAAGCAG 1827
QY 101 SerCysGluGly 104
DB 1828 TCGTGCAGGGC 1839
RESULT 7
ABK49422
ID ABK49422 standard; DNA; 2881 BP.
XX
XX AC ABK49422;
XX
XX 15-JUL-2002 (first entry)
XX
XX DNA encoding human UNC5-like protein NOV1.
XX
XX Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;
KW cell signal processing; metabolic pathway modulation; cancerous tissue;
KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;
KW chromosome 13; gene; ds.
XX
XX Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT CDS 87..2786
FT /*tag= a
FT /product= "Human UNC5-like protein NOV1"
XX
XX WO200229038-A2.
XX
XX 11-APR-2002.
XX
XX 04-OCT-2001; 2001WO-US031377.
XX
XX 04-OCT-2000; 2000US-0237862P.
XX (CURA-) CURAGEN CORP.
XX
XX Herrmann JU, Rastelli L, Shinkets RA;
PI WPI: 2002-340104/37.
DR P-PSDB; AAU79939.
XX
XX Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for
PT treating cardiomyopathy, atherosclerosis, and cancer.
XX
XX Claim 8; Page 7-8; 180pp; English.
XX
XX The present invention relates to a new NOVX polypeptide having a 900
CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)
CC residue amino acid sequence, as given in the specification. The novel
CC polypeptide, and its encoding polynucleotide, are used to treat
CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell
CC signal processing and metabolic pathway modulation, in a human. Detecting
CC the polypeptide or polynucleotide is useful for identifying cancerous
CC tissue. The antibody can be used to treat diabetes or cancer. The host
CC cells can be used to produce non-human transgenic animals useful in drug
CC screening. The present nucleic acid sequence is that of the human UNC5-
CC like NOV1 gene located on chromosome 13. This sequence encodes the human
CC UNC5-like protein NOV1 of the invention
XX
SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.4e-53 Length: 2881
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

```
US-10-624-932C-2_COPY_495_598 (1-104) x ABK49422 (1-2881)
QY 1 ThrSerAenMetThrTyTGlyThrPheAenPheLeuGlyGlyArgLeuMetIleProAen 20
DB 1569 ACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAAT 1628
QY 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyValIleTyxGluIle 40
DB 1629 ACAGGTATCAGCCTCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 1688
QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
DB 1689 TACCTCAGCTGCACACCGGAGACCTGAGTTGCCCTAGCTGGCTGTGCAGACCTG 1748
QY 61 LeuSerProIleValSerCysGlyProProSerProAspSerTrpSerLeuAtqLeuLysLysGln 100
DB 1809 GCTATGGACCACTGTGGGAGCCAGCCCTGACAGCTGGAGCTGGCCTCAAAAAGCAG 1868
QY 101 SerCysGluGly 104
DB 1869 TCGTGGAGGGC 1880
RESULT 8
ADG42568
ID ADG42568 standard; cDNA; 2881 BP.
XX
AC ADG42568;
XX
DT 26-FEB-2004 (first entry)
DE
KW cytotatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
KW NOVX-associated disorder; cancer; human; gene; ss.
OS
XX
XX
XX US2003204052-A1.
XX
XX 30-OCT-2003.
XX
XX 04-OCT-2001; 2001US-00970944.
XX
XX 04-OCT-2000; 2000US-0237862P.
XX
XX (HERR/) HERRMANN J L.
XX (RAST/) RASTELLI L.
XX (SHIM/) SHIMKETS R A.
XX
XX Herrmann Ju, Rastelli L, Shinkets RA;
XX
XX WPI; 2003-900673/82.
XX P-P5DB; ADG42569.
XX
XX New NOVX gene or NOVX-specific antibody, useful for preparing a
XX composition for treating or preventing a NOVX-associated disorder, e.g.,
XX cancer.
XX
XX Claim 9; SEQ ID NO 1; 118pp; English.
XX
XX The invention describes a new isolated polypeptide comprising: a
XX polypeptide or its mature form comprising a sequence not given in the
XX specification; or a variant of (A), where one or more amino acid residues
XX in the variant differs in no more than 15% from the amino acid sequence
XX of the mature form. The pharmaceutical composition may be administered
XX via oral, transdermal, rectal or parenteral route. The polypeptide,
XX nucleic acid or antibody is useful for preparing a composition for
XX treating or preventing a NOVX-associated disorder, e.g., cancer. This
XX
CC sequence encodes a human NOVX protein.
XX
SQ Sequence 2881 BP; 526 A; 987 C; 866 G; 502 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6.4e-53 Length: 2881
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x ADG42568 (1-2881)
QY 1 ThrSerAenMetThrTyTGlyThrPheAenPheLeuGlyGlyArgLeuMetIleProAen 20
DB 1569 ACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAAT 1628
QY 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyxGluIle 40
DB 1629 ACAGGTATCAGCCTCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 1688
QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
DB 1689 TACCTCAGCTGCACACCGGAGACCTGAGTTGCCCTAGCTGGCTGTGCAGACCTG 1748
QY 61 LeuSerProIleValSerCysGlyProProSerProAspSerTrpSerLeuAtqLeuLysLysGln 80
DB 1749 CTGAGTCCCATCGTTAGCTGTGGAGCCAGCCCTGACAGCTGGAGCTGGCCTCAAAAAGCAG 1868
QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuAtqLeuLysLysGln 100
DB 1809 GCTATGGACCACTGTGGGAGCCAGCCCTGACAGCTGGAGCTGGCCTCAAAAAGCAG 1868
QY 101 SerCysGluGly 104
DB 1869 TCGTGGAGGGC 1880
RESULT 9
ADH71649
ID ADH71649 standard; DNA; 2881 BP.
XX
XX ADH71649;
XX
XX 25-MAR-2004 (first entry)
XX
XX Human gene of the invention NOV21u SEQ ID NO:545.
XX
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia.
XX
XX Homo sapiens.
XX
XX WO2003102155-A2.
XX
XX 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
XX
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
XX 06-JUN-2002; 2002US-0386047P.
XX 07-JUN-2002; 2002US-0386376P.
XX 08-JUN-2002; 2002US-0386453P.
XX 09-JUN-2002; 2002US-0386864P.
XX 10-JUN-2002; 2002US-0387016P.
XX 11-JUN-2002; 2002US-0386796P.
XX 12-JUN-2002; 2002US-0386816P.
XX 13-JUN-2002; 2002US-0386931P.
```


CC antilipaemic activity, and may have a use in gene therapy, and as a
 CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
 CC any of the 303 fully defined nucleotide sequences given in the
 CC specification. The polypeptide is useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease. The
 CC polypeptide, polynucleotide and antibody are useful in diagnosing,
 CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
 CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
 CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
 CC further used as hybridisation probes, in chromosome mapping, tissue
 CC typing, preventive medicine, and pharmacogenomics. The present sequence
 CC encodes a NOVX polypeptide of the invention.

SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,4e-53 Length: 2881
 Score: 559.00 Matches: 104
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x ADH71637 (1-2881)

Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPhetLeuGlyArgLeuMetIleProAsn 20
 Db 1569 ACCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAAAT 1628
 Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
 Db 1629 ACAGGTATCAGCCTCCTCATCCCCCAGATGCCATACCCCGAGGAGATCTATGAGATC 1688
 Qy 41 TyrIleThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrIleu 60
 Db 1689 TACCTCAGCTGCACAGCCGAGACGTGAGGTGCCCCCTAGCTGGCTGTGCAGACCCCTG 1748
 Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleIeu 80
 Db 1749 CTGAGTCCCATCTGTTAGCTGTGGACCCCTCGGCTGCTCACCCTGGCCAGTCTATCTCTG 1808
 Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
 Db 1809 GCTATGGACCACTGTGGGGAGCCCGACCCCTGCAGCTGGAGCCTCGGCTCAAAAGCAG 1868
 Qy 101 SerCysGluGly 104
 Db 1869 TCGTCCGAGGGC 1880

RESULT 12

ID ADH71641 standard; DNA; 2881 BP.

AC ADH71641;

DT 25-MAR-2004 (first entry)

XX Human gene of the invention NOV21q SEQ ID NO:537.

XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
 KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
 KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
 KW obesity; diabetes; infectious disease; metabolic syndrome X;
 KW dyslipidaemia.

XX Homo sapiens.

XX WO2003102155-A2.

XX 11-DEC-2003.

XX 03-JUN-2003; 2003WO-US017430.

XX

PR 03-JUN-2002; 2002US-0385120P.
 PR 04-JUN-2002; 2002US-0385784P.
 PR 05-JUN-2002; 2002US-0386041P.
 PR 06-JUN-2002; 2002US-0386376P.
 PR 06-JUN-2002; 2002US-0386453P.
 PR 06-JUN-2002; 2002US-0386864P.
 PR 06-JUN-2002; 2002US-0387016P.
 PR 07-JUN-2002; 2002US-0386796P.
 PR 07-JUN-2002; 2002US-0386816P.
 PR 07-JUN-2002; 2002US-0386931P.
 PR 07-JUN-2002; 2002US-0386942P.
 PR 07-JUN-2002; 2002US-0386971P.
 PR 07-JUN-2002; 2002US-0387262P.
 PR 08-JUN-2002; 2002US-039660P.
 PR 10-JUN-2002; 2002US-0387400P.
 PR 11-JUN-2002; 2002US-0387353P.
 PR 11-JUN-2002; 2002US-0387610P.
 PR 11-JUN-2002; 2002US-0387625P.
 PR 11-JUN-2002; 2002US-0387634P.
 PR 11-JUN-2002; 2002US-0387688P.
 PR 11-JUN-2002; 2002US-0387696P.
 PR 11-JUN-2002; 2002US-0387702P.
 PR 11-JUN-2002; 2002US-0387836P.
 PR 11-JUN-2002; 2002US-0387859P.
 PR 12-JUN-2002; 2002US-0387933P.
 PR 12-JUN-2002; 2002US-0387934P.
 PR 12-JUN-2002; 2002US-0387960P.
 PR 12-JUN-2002; 2002US-0388022P.
 PR 12-JUN-2002; 2002US-0388096P.
 PR 13-JUN-2002; 2002US-0389123P.
 PR 13-JUN-2002; 2002US-0389118P.
 PR 14-JUN-2002; 2002US-0389120P.
 PR 14-JUN-2002; 2002US-0389144P.
 PR 14-JUN-2002; 2002US-0389146P.
 PR 17-JUN-2002; 2002US-0389729P.
 PR 17-JUN-2002; 2002US-0389742P.
 PR 18-JUN-2002; 2002US-0389884P.
 PR 19-JUN-2002; 2002US-0390006P.
 PR 19-JUN-2002; 2002US-0390209P.
 PR 21-JUN-2002; 2002US-0390763P.
 PR 06-AUG-2002; 2002US-0401628P.
 PR 09-AUG-2002; 2002US-0402156P.
 PR 09-AUG-2002; 2002US-0402256P.
 PR 09-AUG-2002; 2002US-0402389P.
 PR 12-AUG-2002; 2002US-0402786P.
 PR 12-AUG-2002; 2002US-0402816P.
 PR 12-AUG-2002; 2002US-0402821P.
 PR 12-AUG-2002; 2002US-0402832P.
 PR 13-AUG-2002; 2002US-0403448P.
 PR 13-AUG-2002; 2002US-0403459P.
 PR 13-AUG-2002; 2002US-0403531P.
 PR 13-AUG-2002; 2002US-0403563P.
 PR 13-AUG-2002; 2002US-0406317P.
 PR 15-AUG-2002; 2002US-040617P.
 PR 26-AUG-2002; 2002US-0406182P.
 PR 26-AUG-2002; 2002US-0406355P.
 PR 27-AUG-2002; 2002US-0406240P.
 PR 12-SEP-2002; 2002US-0410084P.
 PR 20-SEP-2002; 2002US-0412528P.
 PR 23-SEP-2002; 2002US-0412731P.
 PR 30-SEP-2002; 2002US-0414801P.
 PR 30-SEP-2002; 2002US-0414839P.
 PR 30-SEP-2002; 2002US-0414840P.
 PR 30-SEP-2002; 2002US-0414954P.
 PR 09-OCT-2002; 2002US-0417186P.
 PR 09-OCT-2002; 2002US-0417406P.
 PR 23-OCT-2002; 2002US-0420639P.
 PR 28-OCT-2002; 2002US-0421156P.
 PR 31-OCT-2002; 2002US-0422690P.
 PR 01-NOV-2002; 2002US-0423130P.

PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton B, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VV, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Miehra VS;
PI Padigar M, Batturejan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkens RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX WPI: 2004-081935/08.
DR P-FSDB; ADH71642.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 537; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 526 A; 986 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.4e-53 Length: 2881
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x ADH71641 (1-2881)

QY 1 ThrSerAsnMetThrTyrglyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
DB 1569 ACCAGCAACATGACCTATGGACCTTCACTTCTCGGGGGCGGCTGATGATCCCTAAT 1628

QY 21 ThrGlyIleSerLeuLeuLeuProAspAlaIleProArgGlyValIleTyrcGlutIle 40
DB 1629 ACAGGTATCAGGCTCTCTATCCCCCAGATGTCATACCCGAGGGAAGATCTATGAGATC 1689

QY 41 TyrLeuThrLeuHisIleProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
DB 1689 TACCTCAGCTGCACAGCGGAGACGCTGAGTTGCCCTAGCTGGCTGTGCAGACCTG 1748

QY 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
DB 1749 CTGAGTCCCATGCTGTAGCTGTGGACCCCTGCGTCTGCTCACCGGCCGAGTCATCCTG 1808

QY 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuIleValGln 100
DB 1809 GCTATGAGACCACTGTGGGAGGCCAGCCCTGTGACGTGAGCTGCGGCTCAAAAGACG 1869

QY 101 SerCysGluGly 104
DB 1869 TCGTCGAGGGC 1880
RESULT 13
ADH71609
ID ADH71609 standard; DNA; 2881 BP.
XX
XX ADH71609;
AC
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21a SEQ ID NO:505.
XX
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
XX Homo sapiens.
OS
XX WO2003102155-A2.
PN
XX 11-DEC-2003.
PD
XX
XX 03-JUN-2003; 2003WO-US017430.
PF
XX
XX 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 11-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388066P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389146P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390066P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.

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PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417185P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421155P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
XX Catterton E, Crabtree-Bokor JR, Edinger SR, Ellerman K;
XX Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
XX Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
XX Maciachlan T, Malyankar UM, Merick AJ, Millet I, Mishra VS;
XX Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
XX Rieger DK, Rothenberg ME, Sciore P, Shency SG, Shimkets RA;
XX Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
XX Zhong H;
XX WPI; 2004-081935/08.
XX P-PSDB; ADH71629.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
XX treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
XX obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 505; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
XX polypeptide of the invention has cytostatic, immunomodulator,
XX neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
XX anilipaeamic activity, and may have a use in gene therapy, and as a
XX vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
XX any of the 303 fully defined nucleotide sequences given in the
XX specification. The polypeptide is useful in the manufacture of a
XX medicament for treating a syndrome associated with a human disease. The
XX polypeptide, polynucleotide and antibody are useful in diagnosing,
XX treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
XX Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
XX diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
XX further used as hybridisation probes, in chromosome mapping, tissue
XX typing, preventive medicine, and pharmacogenomics. The present sequence
XX encodes a NOVX polypeptide of the invention.
XX
XX Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;
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XX
XX Alignment Scores:
XX Pred. No.: 6.4e-53 Length: 2881
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Db 1569 ACCAGCAACATGACCTATGGACCTTCAACTTCCTCGGGGGCCGGCTGATCCCTAAT 1628
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1629 ACAGGTATCAGCCTCTCTATCCCCCAGATGCCATACCCGAGGGAGAGATCTATGAGATC 1688
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrIleu 60
Db 1689 TACCTCAGCTGCACAAGCCGGAAGACGTGAGGTTCGCCCTAGCTGGCTGTGACAGCCTG 1748
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Db 1749 CTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCTCTGCTCACCCGGCCAGTCATCCTG 1808
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTyrSerLeuArgLeuLysGln 100
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XX AC ADH71629;
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XX DT 25-MAR-2004 (first entry)
XX
XX DE Human gene of the invention NOV21k SEQ ID NO:525.
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XX KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
XX KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX KW obesity; diabetes; infectious disease; metabolic syndrome X,
XX KW dyslipidaemia.
XX
XX OS Homo sapiens.
XX
XX WO2003102155-A2.
XX
XX PD 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
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XX 03-JUN-2002; 2002US-0385120P.
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obesity; diabetes; infectious disease; metabolic syndrome X;

dyslipidaemia.

Homo sapiens.

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03-JUN-2003; 2003WO-US017430.

03-JUN-2002; 2002US-0385120P.

04-JUN-2002; 2002US-0385784P.

05-JUN-2002; 2002US-0386041P.

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Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;

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Gusev VY, Hermann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;

MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;

Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;

Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;

Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;

Zhong H;

WPI; 2004-081935/08.

P-ESDB; ADH71646.

New NOVX polypeptides and nucleic acid molecules useful for preventing or

treating NOVX-associated disorders, e.g. cancer, diabetes, infection or

obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

Example 21; SEQ ID NO 541; 1880pp; English.

The invention relates to a novel isolated polypeptide (NOVX). A

polypeptide of the invention has cytostatic, immunomodulator,

neuroprotective, anorectic, antidiabetic, antimicrobial, and

antitumorigenic activity, and may have a use in gene therapy, and as a

vaccine. The polypeptides are encoded by NOVX polynucleotides comprising

any of the 303 fully defined nucleotide sequences given in the

specification. The polypeptide is useful in the manufacture of a

medicament for treating a syndrome associated with a human disease. The

polypeptide, polynucleotide and antibody are useful in diagnosing,

treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,

Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious

diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are

further used as hybridisation probes, in chromosome mapping, tissue

typing, preventive medicine, and pharmacogenomics. The present sequence

encodes a NOVX polypeptide of the invention.

Sequence 2881 BP; 526 A; 986 C; 868 G; 501 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.4e-53 Length: 2881

Score: 559.00 Matches: 104

Percent Similarity: 100.00% Conservativeness: 0

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Qy 21 ThrGlyIleSerLeuLeuIleProAspAlaIleProArgGlyLysIleTyrGluIle 40

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Qy      81   |||||AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGln 100
Db      1809  |||||GCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCCTGGCCCTCAAAAAGCAG 1868
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20	163.5	29.2	7888	4	US-09-919-497-48	Sequence 48, Appl
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25	132.5	23.7	966	4	US-09-969-532-23	Sequence 23, Appl
26	132.5	23.7	999	4	US-09-969-532-21	Sequence 21, Appl
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31	132.5	23.7	1701	4	US-09-969-532-3	Sequence 3, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/08808982
; Patent No. 5919271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1787 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cdna
US-08-808-982-2

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; Sequence 2, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627

;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1787 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cdna
US-09-306-902A-2

Alignment Scores:
Pred. No.: 1.14e-61 Length: 1787
Score: 553.00 Matches: 103
Percent Similarity: 99.04% Conservativeness: 0
Best Local Similarity: 99.04% Mismatches: 1
Query Match: 98.93% Indels: 0
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Db 519 ACAGGAATCAGCTCTCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 578
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Db 579 TACCTCAGCTGCAACAGCGGAGACGTGAGGTTGCCCTAGCTGGCTGTGCAGACCCCTG 638
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Db 639 CTGAGTCCCATCGTTAGCTGTGGACCCCTGCGCTCTGCTACCCGCCAGTATCTCTG 698
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RESULT 3
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; Sequence 1, Application US/08808982
; Patent No. 593271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```


APPLICATION NUMBER: US/08/808,982

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UC96-217

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3014 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-808-982-1

Alignment Scores:

Pred. No.:	2,42e-61	Length:	3014
Score:	553.00	Matches:	102
Percent Similarity:	99.04%	Conservative:	1
Best Local Similarity:	98.08%	Mismatches:	1
Query Match:	98.93%	Indels:	0
DB:	2	Gaps:	0

US-10-624-932C-2_COPY_495_598 (1-104) x US-08-808-982-1 (1-3014)

Qy	1	ThrSerAsnMetThrTyrGlyThrPheAsnPhelLeuGlyArgLeuMetIleProAsn	20
Db	1483	ACCGGATCAGCTTCTTCAACCTTACGGGCGCGGCTGATGATCCCTAAT	1542
Qy	21	ThrGlyIleSerLeuLeuIleProAspAlaIleProArgGlyLysIleTyrGluIle	40
Db	1543	ACGGGATCAGCTTCTTCAACCTTACGGGCGCGGCTGATGATCCCTAAT	1602
Qy	41	TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu	60
Db	1603	TACCTCACCTGCACAGCCAGAGACGTGAGTTGCCCTAGCTGGCTGTCCAGACCTG	1662
Qy	61	LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu	80
Db	1663	CTGAGTCAGTCGTAGCTGTGGGCCCCCAGAGCTGCTGCTCACCCGCCAGTCATCCTT	1722
Qy	81	AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln	100
Db	1723	GCAATGGACCACTGTGGAGAGCCCGCCCTGACAGCTGGAGTCTGGGCTCATAAAGCAG	1782
Qy	101	SerCysGluGly	104
Db	1783	TCCTGCGAGGGC	1794

RESULT 4

US-306-902A-1

Sequence 1, Application US/09306902A

Patent No. 627585

GENERAL INFORMATION:

APPLICANT: Tessier-Lavigne, Marc

Leonardo, E. David

Hink, Lindsey

Masu, Masayuki

Kazuko, Keino-Masu

TITLE OF INVENTION: Netrin Receptors

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/306,902A

FILING DATE: 07-May-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UC96-217

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3014 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-306-902A-1

Alignment Scores:

Pred. No.:	2,42e-61	Length:	3014
Score:	553.00	Matches:	102
Percent Similarity:	99.04%	Conservative:	1
Best Local Similarity:	98.08%	Mismatches:	1
Query Match:	98.93%	Indels:	0
DB:	3	Gaps:	0

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-306-902A-1 (1-3014)

Qy	1	ThrSerAsnMetThrTyrGlyThrPheAsnPhelLeuGlyArgLeuMetIleProAsn	20
Db	1483	ACCGGATCAGCTTCTTCAACCTTACGGGCGCGGCTGATGATCCCTAAT	1542
Qy	21	ThrGlyIleSerLeuLeuIleProAspAlaIleProArgGlyLysIleTyrGluIle	40
Db	1543	ACGGGATCAGCTTCTTCAACCTTACGGGCGCGGCTGATGATCCCTAAT	1602
Qy	41	TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu	60
Db	1603	TACCTCACCTGCACAGCCAGAGACGTGAGTTGCCCTAGCTGGCTGTCCAGACCTG	1662
Qy	61	LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu	80
Db	1663	CTGAGTCAGTCGTAGCTGTGGGCCCCCAGAGCTGCTGCTCACCCGCCAGTCATCCTT	1722
Qy	81	AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln	100
Db	1723	GCAATGGACCACTGTGGAGAGCCCGCCCTGACAGCTGGAGTCTGGGCTCATAAAGCAG	1782
Qy	101	SerCysGluGly	104
Db	1783	TCCTGCGAGGGC	1794

RESULT 5

US-09-949-016-4794

Sequence 4794, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC96-217
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2831 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-306-902A-3

Alignment Scores:			
Pred. No.:	1,45e-25	Length:	2831
Score:	277.00	Matches:	55
Percent Similarity:	69.23%	Conservative:	17
Best Local Similarity:	52.88%	Mismatches:	30
Query Match:	49.55%	Indels:	2
DB:	3	Gaps:	2

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-306-902A-3 (1-2831)

Qy 2 SerAenMetThrTyTGlyThrPheAsnPhelLeuGlyGlyArgLeuMetIleProAsnThr 21
Db 1618 AGCAGCAGTCGTCAGTGGCACCTTTGGTTGGCTGGGTGGGAGCGTCACCATTCCTCCGGGCACA 1677
Qy 22 GlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyxGluIleTyx 41
Db 1678 GGGTGCACCTGTTGGTACCAAAATGAGGCCATTCCCGAGGGCAAGTTCTATGACTTGTAT 1737
Qy 42 LeuThrLeuHisLysProGluAspValArgLeuProLeuAla---GlyCysGlnThrLeu 60
Db 1738 CTAGGTATCAACAGACTGAAAGCACC---CTCCCACTTTCGGAAGGTTCCAGACAGTA 1794
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1795 TTGAGCCCTCGGTGACCTGCGGGCCACAGGGCCCTCTCCCTGTGCGGCCCTGTGTCTCTC 1854
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1855 ACTGTGCCCCACTGTGCTGAAGTCATTCCCGGAGACTGGAATCTTCCAGCTCAAGACCCAG 1914
Qy 101 SerCysGluGly 104
Db 1915 GCCCATCAGGGC 1926

RESULT 8
US-09-969-532-31
; Sequence 31, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodir
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-31

Alignment Scores:
Pred. No.:

1.91e-21 Length: 1968
Score: 243.50 Matches: 47
Percent Similarity: 66.35% Conservative: 22
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 43.56% Indels: 1
DB: 4 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-31 (1-1968)

Qy 1 ThrSerAenMetThrTyTGlyThrPheAsnPhelLeuGlyGlyArgLeuMetIleProAsn 20
Db 724 ACAGAACTGAGGACAACTGGTCTTTGGCCATTTAGGGGGCGCTTAGTATGCAAAAT 783
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyxGluIle 40
Db 784 ACAGGGTGAGCTTACTCATACACACGGTCCCATCCAGAGGAGAAATCTTGGGAGATT 843
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 844 TATATGTCATCAACCAAGGTGAACCC---AGCCTCCAGTCAGATGGCTCTGAGGTGCTC 900
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 901 CTGAGTCTCTGAAGTCACCTGTGGTCTCCAGACATGATCGTCACCACTCCCTTTGCATTG 960
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 961 ACCATCCCGCACTGTGCAGATGTCAGTTCTGAGCATTCGAATATCCATTTAAAGAAGAGG 1020
Qy 101 SerCysGluGly 104
Db 1021 ACACAGCAGGGC 1032

RESULT 9

US-09-969-532-29
; Sequence 29, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-29

Alignment Scores:
Pred. No.:

1.95e-21 Length: 2001
Score: 243.50 Matches: 47
Percent Similarity: 66.35% Conservative: 22
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 43.56% Indels: 1
DB: 4 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-29 (1-2001)

Qy 1 ThrSerAenMetThrTyTGlyThrPheAsnPhelLeuGlyGlyArgLeuMetIleProAsn 20
Db 757 ACAGAACTGAGGACAACTGGTCTTTGGCCATTTAGGGGGCGCTTAGTATGCAAAAT 816
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyxGluIle 40
Db 817 ACAGGGTGAGCTTACTCATACACACGGTCCCATCCAGAGGAGAAATCTTGGGAGATT 876

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Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 877 TATATGTCCTCAACCAAGGTGAACCC---AGCTCCAGTCAGATGGCTCTGAGGTGCTC 933
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 934 CTGAGTCTCTGAAGTCACCTGTGGTCTCCAGACATGATCGTCACCACTCCCTTTGCATTG 993
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 994 ACCATCCGGCACTGTCAGATGTCAAGTCTTGAGCATTTGGAATATCCATTTAAAGAAGAGG 1053
Qy 101 SerCysGluGly 104
Db 1054 ACACAGCAGGCGC 1065

RESULT 10
US-09-969-532-27
; Sequence 27, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-27

Alignment Scores:
Pred. No.: 1.96e-21 Length: 2010
Score: 243.50 Matches: 47
Percent Similarity: 66.35% Conservative: 22
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 43.56% Indels: 1
Gaps: 4
DB: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-27 (1-2010)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 766 ACAGAACTGAGGACAACTGGTGTCTTTGGCCATTAGGGGGCGCTTAGTAATGCCAAAT 825
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 826 ACAGGGGTGAGCTTACTCATACCAACAGCGTGCCATCCAGACATGATCGTCACCACTCCCTTTGCATTG 885
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 886 TATATGTCCTCAACCAAGGTGAACCC---AGCTCCAGTCAGATGGCTCTGAGGTGCTC 942
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 943 CTGAGTCTCTGAAGTCACCTGTGGTCTCCAGACATGATCGTCACCACTCCCTTTGCATTG 1002
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1003 ACCATCCGGCACTGTCAGATGTCAAGTCTTGAGCATTTGGAATATCCATTTAAAGAAGAGG 1062
Qy 101 SerCysGluGly 104
Db 1063 ACACAGCAGGCGC 1074

RESULT 11
US-09-969-532-25
```

```
; Sequence 25, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 2043
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-25

Alignment Scores:
Pred. No.: 2.01e-21 Length: 2043
Score: 243.50 Matches: 47
Percent Similarity: 66.35% Conservative: 22
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 43.56% Indels: 1
Gaps: 4
DB: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-25 (1-2043)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 799 ACAGAACTGAGGACAACTGGTGTCTTTGGCCATTAGGGGGCGCTTAGTAATGCCAAAT 858
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 859 ACAGGGGTGAGCTTACTCATACCAACAGCGTGCCATCCAGACATGATCGTCACCACTCCCTTTGCATTG 918
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 919 TATATGTCCTCAACCAAGGTGAACCC---AGCTCCAGTCAGATGGCTCTGAGGTGCTC 975
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 976 CTGAGTCTCTGAAGTCACCTGTGGTCTCCAGACATGATCGTCACCACTCCCTTTGCATTG 1035
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1036 ACCATCCGGCACTGTCAGATGTCAAGTCTTGAGCATTTGGAATATCCATTTAAAGAAGAGG 1095
Qy 101 SerCysGluGly 104
Db 1096 ACACAGCAGGCGC 1107

RESULT 12
US-09-969-532-15
; Sequence 15, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-15
```

Alignment Scores:
Pred. No.: 2,95e-21 Length: 2661
Score: 243.50 Matches: 47
Percent Similarity: 66.35% Conservative: 22
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 43.56% Indels: 1
DB: 4 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-15 (1-2661)

Qy 1 ThrSerAsnMetThrTyGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1417 ACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCAAAAT 1476

Qy 21 ThrGlyIleSerLeuLeuIleProAspAlaIleProArgGlyLysIleTyRGlutle 40
Db 1477 ACAGGGGTGAGCTTACTATACCACACCGTGCATCCAGAGGAGAAATTCITGGGAGATT 1536

Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1537 TATATGTCCATCAACCAAGGTGAACCC---AGCCTCCAGTCAGATGGCTCTGAGGTGCTC 1593

Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 1594 CTGAGTCCTGAAGTCACCTGTGTCTCCAGACATGATCGTCACCACTCCCTTTGCATTG 1653

Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTyrSerLeuArgLeuLysGln 100
Db 1654 ACCATCCCGCACTGTGCAGATGTCAGTTCTTGAGCATTTGGAATATCCATTTAAAGAGAGG 1713

Qy 101 SerCysGluGly 104
Db 1714 ACACAGCAGGGC 1725

RESULT 13
US-09-969-532-13
; Sequence 13, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodi
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969.532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-13

Alignment Scores:
Pred. No.: 3e-21 Length: 2694
Score: 243.50 Matches: 47
Percent Similarity: 66.35% Conservative: 22
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 43.56% Indels: 1
DB: 4 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-13 (1-2694)

Qy 1 ThrSerAsnMetThrTyGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1450 ACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCAAAAT 1509

Qy 21 ThrGlyIleSerLeuLeuIleProAspAlaIleProArgGlyLysIleTyRGlutle 40
Db 1510 ACAGGGGTGAGCTTACTATACCACACCGTGCATCCAGAGGAGAAATTCITGGGAGATT 1569

Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1570 TATATGTCCATCAACCAAGGTGAACCC---AGCCTCCAGTCAGATGGCTCTGAGGTGCTC 1626

Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 1627 CTGAGTCCTGAAGTCACCTGTGTCTCCAGACATGATCGTCACCACTCCCTTTGCATTG 1686

Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTyrSerLeuArgLeuLysGln 100
Db 1687 ACCATCCCGCACTGTGCAGATGTCAGTTCTTGAGCATTTGGAATATCCATTTAAAGAGAGG 1746

Qy 101 SerCysGluGly 104
Db 1747 ACACAGCAGGGC 1758

RESULT 14
US-09-969-532-11
; Sequence 11, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodi
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969.532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-11

Alignment Scores:
Pred. No.: 3.01e-21 Length: 2703
Score: 243.50 Matches: 47
Percent Similarity: 66.35% Conservative: 22
Best Local Similarity: 45.19% Mismatches: 34
Query Match: 43.56% Indels: 1
DB: 4 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-11 (1-2703)

Qy 1 ThrSerAsnMetThrTyGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1459 ACAGAACTGAGGACAACTGGTGTCTTTGGCCATTTAGGGGGCGCTTAGTAATGCAAAAT 1518

Qy 21 ThrGlyIleSerLeuLeuIleProAspAlaIleProArgGlyLysIleTyRGlutle 40
Db 1519 ACAGGGGTGAGCTTACTATACCACACCGTGCATCCAGAGGAGAAATTCITGGGAGATT 1578

Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1579 TATATGTCCATCAACCAAGGTGAACCC---AGCCTCCAGTCAGATGGCTCTGAGGTGCTC 1635

Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 1636 CTGAGTCCTGAAGTCACCTGTGTCTCCAGACATGATCGTCACCACTCCCTTTGCATTG 1695

Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTyrSerLeuArgLeuLysGln 100
Db 1696 ACCATCCCGCACTGTGCAGATGTCAGTTCTTGAGCATTTGGAATATCCATTTAAAGAGAGG 1755

Qy 101 SerCysGluGly 104
Db 1756 ACACAGCAGGGC 1767

RESULT 15

```
US-09-969-532-9
; Sequence 9, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-9

Alignment Scores:
Pred. No.:      3.07e-21      Length:      2736
Score:          243.50      Matches:      47
Percent Similarity: 66.35%      Conservative: 22
Best Local Similarity: 45.19%      Mismatches:  34
Query Match:      43.56%      Indels:      1
DB:               4          Gaps:      1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-969-532-9 (1-2736)

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Db      1492 ACAGAACTGAGGACAACTGGTGCTTTGGCCATTAGGGGGCCCTTAGTAATGCCAAT 1551

Qy      21  ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db      1552 ACAGGGGTGAGCTTACTACATACCACACGGTGCCATCCAGAGGAGAAATTCCTGGGAGATT 1611

Qy      41  TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrIleu 60
Db      1612 TATATGTCCATCAACCAAGGTGAACCC---AGCCTCCAGTCAGATGGCTCTGAGGTGCTC 1668

Qy      61  LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db      1669 CTGAGTCTTGAGTCACTGTGGTCTCCAGACATGATCGTACCACCTCCCTTTGCATTG 1728

Qy      81  AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db      1729 ACCATCCCGCACTGTGCAGATGTCAAGTCTTGAGCATTTGGAATATCCATTTAAAGAAGAGG 1788

Qy      101 SerCysGluGly 104
Db      1789 ACACAGCAGGGC 1800
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Search completed: September 9, 2005, 09:51:53
Job time : 172.773 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 9, 2005, 04:41:16 ; Search time 1037.83 Seconds
(without alignments)
658.098 Million cell updates/sec

Title: US-10-624-932c-2_COPY_495_598

Perfect score: 559

Sequence: 1 TSNMTYGTNFGLRLMPN.....CGEFPSPWSLRLKKQSCG 104

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published_Applications_NA -QFM=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=DIAGONAL
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -WAP=US10624932 @cgn1_1.989 @rnatat_08092005_161709_15882
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubna/US06_NEW_PUB.seq.*
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- 5: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubna/US08_NEW_PUB.seq.*
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- 9: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/1/pubna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubna/US10J_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	559	100.0	2752	10	US-09-918-779-1	Sequence 1, Appli
2	559	100.0	2752	18	US-10-624-932-1	Sequence 1, Appli
3	559	100.0	2881	10	US-09-970-944-1	Sequence 1, Appli
4	559	100.0	3561	20	US-10-643-795A-77	Sequence 77, Appl
5	559	100.0	3561	21	US-10-948-518-77	Sequence 13, Appl
6	559	100.0	3580	17	US-10-311-623-13	Sequence 2, Appli
7	553	98.9	1787	10	US-09-933-261-2	Sequence 2, Appli
8	553	98.9	1787	14	US-10-256-702-2	Sequence 15, Appl
9	553	98.9	2697	16	US-10-240-154-15	Sequence 1, Appli
10	553	98.9	3014	10	US-09-933-261-1	Sequence 1, Appli
11	553	98.9	3014	14	US-10-256-702-1	Sequence 1, Appli
12	503	90.0	1321	18	US-10-296-115-365	Sequence 365, App
C 13	393.5	70.4	9582	9	US-09-764-861-62	Sequence 62, Appl
C 14	393.5	70.4	9582	10	US-09-764-861-62	Sequence 62, Appl
C 15	393.5	70.4	9582	14	US-10-115-928-62	Sequence 62, Appl
C 16	393.5	70.4	18772	9	US-09-764-861-63	Sequence 63, Appl
C 17	393.5	70.4	18772	10	US-09-764-861-63	Sequence 63, Appl
C 18	393.5	70.4	18772	14	US-10-115-928-63	Sequence 63, Appl
19	287	51.3	1026	9	US-09-764-870-171	Sequence 171, App
20	287	51.3	1026	14	US-10-125-540-171	Sequence 171, App
21	287	51.3	2406	17	US-10-108-260A-239	Sequence 239, App
22	287	51.3	2406	20	US-10-723-860-5786	Sequence 5786, Ap
23	287	51.3	2860	17	US-10-087-684-1	Sequence 1, Appli
24	287	51.3	2860	17	US-10-087-684-3	Sequence 3, Appli
25	287	51.3	2860	17	US-10-218-779-1	Sequence 1, Appli
26	287	51.3	2860	17	US-10-218-779-3	Sequence 3, Appli
27	287	51.3	2895	18	US-10-032-417-37	Sequence 37, Appl
28	287	51.3	2995	11	US-09-972-211-55	Sequence 55, Appl
29	287	51.3	2995	18	US-10-096-625-55	Sequence 55, Appl
30	287	51.3	3485	9	US-09-816-828-18	Sequence 18, Appl
31	287	51.3	3501	17	US-10-295-027-1123	Sequence 1123, Ap
32	287	51.3	3884	14	US-10-028-072-145	Sequence 145, App
33	287	51.3	3884	14	US-10-140-808-145	Sequence 145, App
34	287	51.3	3884	14	US-10-121-049-145	Sequence 145, App
35	287	51.3	3884	14	US-10-123-904-145	Sequence 145, App
36	287	51.3	3884	14	US-10-140-470-145	Sequence 145, App
37	287	51.3	3884	14	US-10-175-746-145	Sequence 145, App
38	287	51.3	3884	14	US-10-176-918-145	Sequence 145, App
39	287	51.3	3884	14	US-10-176-921-145	Sequence 145, App
40	287	51.3	3884	14	US-10-137-865-145	Sequence 145, App
41	287	51.3	3884	14	US-10-140-474-145	Sequence 145, App
42	287	51.3	3884	14	US-10-142-431-145	Sequence 145, App
43	287	51.3	3884	14	US-10-143-114-145	Sequence 145, App
44	287	51.3	3884	14	US-10-142-419-145	Sequence 145, App
45	287	51.3	3884	14	US-10-123-262-145	Sequence 145, App

ALIGNMENTS

RESULT 1
US-09-918-779-1
; Sequence 1, Application US/09918779
; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William

APPLICANT: Alsobrook, John
APPLICANT: Lepley, Denise
APPLICANT: Burgess, Catherine
APPLICANT: Gerlach, Valerie
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-074 US
CURRENT APPLICATION NUMBER: US/09/918,779
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/221,409
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/222,840
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,752
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,762
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,770
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,769
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/225,146
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,392
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/263,662
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/281,645
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2752
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-779-1

Alignment Scores:
Pred. No.: 2,05e-66 Length: 2752
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

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Db 1648 TACTCTACGCTGCAACAGCCGGAAGACGTGAGGTGGCCCTAGCTGGCTGCAGACCCCTG 1707

Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1708 CTGAGTCCCATCTGTTAGTGTGGACCCCTCGGCTGCTCTCACCCGCGCACTATCTCTG 1767

Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
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Qy 101 SerCysGluGly 104
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RESULT 2
US-10-624-932-1
Sequence 1, Application US/10624932
Publication No. US20040096877A1
GENERAL INFORMATION:
APPLICANT: Taupier, Raymond
APPLICANT: Padigaru, Muralidhara
APPLICANT: Rastelli, Luca
APPLICANT: Spaderna, Steven
APPLICANT: Shinkets, Richard
APPLICANT: Zerhusen, Bryan
APPLICANT: Spytek, Kimberly
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Gusev, Vladimir
APPLICANT: Grosse, William
APPLICANT: Alsobrook, John
APPLICANT: Lepley, Denise
APPLICANT: Burgess, Catherine
APPLICANT: Gerlach, Valerie
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John
APPLICANT: Stone, David
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-074 US
CURRENT APPLICATION NUMBER: US/10/624,932
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: 09/918,779
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/221,409
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/222,840
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,752
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,762
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,770
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/223,769
PRIOR FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/225,146
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,392
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/225,470
PRIOR FILING DATE: 2000-08-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2752
TYPE: DNA
ORGANISM: Homo sapiens
US-10-624-932-1

Alignment Scores:
Pred. No.: 2,05e-66 Length: 2752
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

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Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1648 TACCTCAGCCTGCACAAGCCGAGACGCTGAGGTTGCCCTAGCTGGCTGTCCAGACCCCTG 1707
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 1708 CTGAGTCCCATCGTTAGCTGTGGACCCCTCGCGTCTGCTCACC CGGCCAGTCACTCCTG 1767
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1768 GCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCCTCGGCTCAAAAAGCAG 1827
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Db 1828 TCGTGCAGGGGC 1839

RESULT 3
US-09-970-944-1
; Sequence 1, Application US/09970944
; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same an
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 60/237,862
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2881
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-944-1

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Pred. No.: 2,186-66 Length: 2881
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

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Db 1629 ACAGGTATCAGCCTCTCTATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 1688
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1689 TACCTCAGCCTGCACAAGCCGAGACGCTGAGGTTGCCCTAGCTGGCTGTCCAGACCCCTG 1748
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Qy 101 SerCysGluGly 104
Db 1869 TCGTGCAGGGGC 1880

RESULT 4
US-10-643-795A-77
; Sequence 77, Application US/10643795A
; Publication No. US20040241703A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/643,795A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-643-795A-77

Alignment Scores:
Pred. No.: 2,86e-66 Length: 3561
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x US-10-643-795A-77 (1-3561)
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Qy 21 ThrGlyIleSerLeuLeuProAspAlaIleProAsgGlyValIleTyrGluIle 40
Db 1378 ACAGGAATCAGCCTCTCTATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 1437
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1438 TACCTCAGCCTGCACAGCCGAGACGCTGAGGTTGCCCTAGCTGGCTGTCCAGACCCCTG 1497
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db 1498 CTGAGTCCCATCGTTAGCTGTGGACCCCTCGCGTCTGCTCACC CGGCCAGTCACTCCTG 1557
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
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Db 1558 GCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCCTCAAAAAGCAG 1617
Qy 101 SerCysGluGly 104
Db 1618 TCGTGGGAGGCG 1629
RESULT 5
US-10-948-518-77
; Sequence 77, Application US/10948518
; Publication No. US2005006492A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITL OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/948,518
; PRIOR FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: US/10/643,795
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-948-518-77
Alignment Scores:
Pred. No.: 2,86e-66 Length: 3561
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x US-10-948-518-77 (1-3561)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1318 ACCAGCAACATGACCTATGGAGCCTTCAACTTCTCGGGGGCCGGCTGATGATCCCTAAT 1377
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1378 ACAGGAATCAGCTCTCTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 1437
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1438 TACCTCAGCTGCAACAGCCGGAAGAGCGTGAGGTGGCCCTAGCTGGCTGTGCAGACCTG 1497
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleIleu 80
Db 1498 CTGAGTCCCAATCGTAGCTGTGGAGCCCTCGGCTCTCTGCTACCCGCGCAGTATCCTG 1557
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100

Db 1558 GCTATGGACCACTGTGGGGAGCCAGCCCTGACAGCTGGAGCCTCAAAAAGCAG 1617
Qy 101 SerCysGluGly 104
Db 1618 TCGTGGGAGGCG 1629
RESULT 6
US-10-311-623-13
; Sequence 13, Application US/10311623
; Publication No. US20040023244A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Dannel B.
; APPLICANT: TANG, Y. Tom; LAU, Preeti G.
; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAPALIA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.
; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PE-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 3580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CB1
US-10-311-623-13
Alignment Scores:
Pred. No.: 2,88e-66 Length: 3580
Score: 559.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x US-10-311-623-13 (1-3580)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 1318 ACCAGCAACATGACCTATGGAGCCTTCAACTTCTCGGGGGCCGGCTGATGATCCCTAAT 1377
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db 1378 ACAGGAATCAGCTCTCTCATCCCCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 1437
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1438 TACCTCAGCTGCAACAGCCGGAAGAGCGTGAGGTGGCCCTAGCTGGCTGTGCAGACCTG 1497
Qy 61 LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleIleu 80
Db 1498 CTGAGTCCCAATCGTAGCTGTGGAGCCCTCGGCTCTCTGCTACCCGCGCAGTATCCTG 1557

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Qy      81  AlawetAspHisCysGlyGluProSerProAspSerTrpSerIleuArgLeuLysLysGln 100
      |||||
Db      1558  GCTATGACCACCTGTGGGGAGCCCGACGCTGGAGCTGGCGCCTCAAAAAGCAG 1617
      |||||
Qy      101  SerCysGluGly 104
      |||||
Db      1618  TCGTGGGAGGC 1629
      |||||

RESULT 7
US-09-933-261-2
; Sequence 2, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
;             Leonardo, E. David
;             Hink, Lindsey
;             Masu, Masayuki
;             Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1787 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-933-261-2

Alignment Scores:
Pred. No.:      7.93e-66      Length:      1787
Score:          553.00      Matches:      103
Percent Similarity: 99.04%      Conservative: 0
Best Local Similarity: 99.04%      Mismatches: 1
Query Match:      98.93%      Indels:      0
DB:              10      Gaps:      0

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-933-261-2 (1-1787)

Qy      1  Thr-Ser-Asn-Met-Thr-Tyr-Gly-Thr-Phe-Asn-Phe-Leu-Gly-Gly-Arg-Leu-Met-Ile-Pro-Asn 20
      |||||
Db      459  ACCAGCAACATGACCTATGGAGCCTTCACTTCTCGGGGGCGGCTGATGATCCCTAAT 518
      |||||
Qy      21  Thr-Gly-Ile-Ser-Leu-Leu-Ile-Pro-Pro-Asp-Ala-Ile-Pro-Arg-Gly-Ile-Tyr-Glu-Ile 40
      |||||

```

Db	519	ACAGGAATCAGCTCTCTCATCTCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC	578
Qy	41	TyrLeuThrLeuHisIysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu	60
Db	579	TACTCAGCTGCACAAAGCCGGAAGACGTGAGGTTGCCCTTAGCTGGCTGTGCAGACCCTG	638
Qy	61	LeuSerProIleValSerCysGlyProProClyValLeuLeuThrArgProValIleLeu	80
Db	639	CTGAGTCCCATCGTTAGCTGTGGACCCCTGCGCTTCCTCAGCCCGCCAGTCATCCTG	698
Qy	81	AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuIysIysGln	100
Db	699	GCTATGACCACTGTGGGGAGCCCGACCCCTGACAGCTGGAGCCTGGCCCTCAAAAAGCAG	758
Qy	101	SerCysGluGly 104	
Db	759	TCGTGCGAGGGA 770	
RESULT 8			
US-10-256-702-2			
; Sequence 2, Application US/10256702			
; Publication No. US20030059859A1			
; GENERAL INFORMATION:			
; APPLICANT: Tessier-Lavigne, Marc			
; Leonardo, E. David			
; Hink, Lindsey			
; Masu, Masayuki			
; Kazuko, Keino-Masu			
; TITLE OF INVENTION: Netrin Receptors			
; NUMBER OF SEQUENCES: 8			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP			
; STREET: 268 BUSH STREET, SUITE 3200			
; CITY: SAN FRANCISCO			
; STATE: CALIFORNIA			
; COUNTRY: USA			
; ZIP: 94104			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent in Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/10/256.702			
; FILING DATE: 27-Sep-2002			
; CLASSIFICATION: <Unknown>			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US/09/933,261			
; FILING DATE: 20-Aug-2001			
; APPLICATION NUMBER: 08/808,982			
; FILING DATE: <Unknown>			
; ATTORNEY/AGENT INFORMATION:			
; NAME: OSMAN, RICHARD A			
; REGISTRATION NUMBER: 36,627			
; REFERENCE/DOCKET NUMBER: UC96-217			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (415) 343-4341			
; TELEFAX: (415) 343-4342			
; INFORMATION FOR SEQ ID NO: 2:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 1787 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: linear			
; MOLECULE TYPE: cDNA			
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:			
US-10-256-702-2			
Alignment Scores:			
Pred. No.: 7.93e-66 Length: 1787			
Score: 553.00 Matches: 103			
Percent Similarity: 99.04% Conservative: 0			
Best Local Similarity: 99.04% Mismatches: 1			

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Query Match: 98.93% Indels: 0
DB: 14 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x US-10-256-702-2 (1-1787)

Qy 1 ThrSerAenMetThrTyrglyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 459 ACCAGCAACATGACTATGGACCTTCACTTCCTCGGGGCGCGCTGATGATCCCTAAT 518
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluile 40
Db 519 ACAGGAATCAGCTCCTCATCCGCCAGATGCCATACCCGAGGGAAGATCTATGAGATC 578
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 579 TACCTCAGCTGCAAGCCGAGAGAGCTGAGGTGCCCCCTAGCTGGCTGTCAGACCCCTG 638
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 639 CTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCTCTCACCAGCCAGTCATCTG 698
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 699 GCTATGGACCACTGTGGGAGCCAGCCCTCACAGCTGGAGCTGGCCCTCAAAAAGCAG 758
Qy 101 SerCysGluGly 104
Db 759 TCGTGGCAGGGA 770

RESULT 9
US-10-154-15
; Sequence 15, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; FILE REFERENCE: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CRFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240.154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 2697
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15
Alignment Scores:
Pred. No.: 1.35e-65 Length: 2697
Score: 553.00 Matches: 102
Percent Similarity: 99.04% Conservative: 1
Best Local Similarity: 98.08% Mismatches: 1
Query Match: 98.93% Indels: 0
DB: 16 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x US-10-240-154-15 (1-2697)

Qy 1 ThrSerAenMetThrTyrglyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 1483 ACCAGCAACATGCGCTACGGACCTTCACTTCCTCGGGGCGCGCTGATGATCCCTAAT 1542
Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluile 40
Db 1543 ACGGGGATCAGCTCCTCATACCCCGGATGCCATCCCGAGGGAAGATCTACGAGATC 1602
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1603 TACCTCAGCTGCAAGCCGAGAGAGCTGAGGTGCCCCCTAGCTGGCTGTCAGACCCCTG 1662

Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db 1663 CTGAGTCCCATCGTTAGCTGTGGGCCCCCAGGAGTCTCTGCTCACCCGCGCAGTCATCCTT 1722
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1723 GCATGAGCACCTGTGAGAGAGCCGCTGACAGCTGGAGTCTGGCGCTCAAAAAGCAG 1782
Qy 101 SerCysGluGly 104
Db 1783 TCCTGGCAGGGC 1794

RESULT 10
US-09-933-261-1
; Sequence 1, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933.261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-933-261-1
Alignment Scores:
Pred. No.: 1.56e-65 Length: 3014
Score: 553.00 Matches: 102
Percent Similarity: 99.04% Conservative: 1
Best Local Similarity: 98.08% Mismatches: 1
Query Match: 98.93% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-933-261-1 (1-3014)

Qy 1 ThrSerAenMetThrTyrglyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 1783 TCCTGGCAGGGC 1794
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Db 1483 ACCAGCAATGCGCTACGGGACCTTCAACTTCCTCGGGGGCCGCTGATGATCCCTAAT 1542
Qy 21 ThrGlyileSerLeuLeuileProAspAlaileProArgGlyLysileTyrGluile 40
Db 1543 ACGGGGATCAGCTCTCTATACCCCGGATGCCATCCCGGAGGAAAGATCTACGAGATC 1602
Qy 41 TyrLeuThrLeuHisLysProGluaspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1603 TACCTCACATGCAACAGCCAGACGCTGAGGTTGCCCTAGCTGGCTGTTCAGACCCCTG 1662
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValileLeu 80
Db 1663 CTGAGTCAGTCGTTAGCTGTGGGCCCCCAGGAGTCCCTGCTCACC CGGCGCAGTCATCCTT 1722
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1723 GCAATGGACCACTGTGGAGAGCCAGCCCTGCACAGCTGGAGTCTGGGCTCAAAAAGCAG 1782
Qy 101 SerCysGluGly 104
Db 1783 TCCTGCGAGGGC 1794

RESULT 11

US-10-256-702-1
; Sequence 1, Application US/10256702
; Publication No. US20030059859A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/256,702
; FILING DATE: 27-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-256-702-1

Alignment Scores:

Pred. No.: 1,56e-65 Length: 3014
Score: 553.00 Matches: 102
Percent Similarity: 99.04% Conservative: 1
Best Local Similarity: 98.08% Mismatches: 1
Query Match: 98.93% Indels: 0
DB: 14 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x US-10-256-702-1 (1-3014)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 1483 ACCAGCAATGCGCTACGGGACCTTCAACTTCCTCGGGGGCCGCTGATGATCCCTAAT 1542
Qy 21 ThrGlyileSerLeuLeuileProAspAlaileProArgGlyLysileTyrGluile 40
Db 1543 ACGGGGATCAGCTCTCTATACCCCGGATGCCATCCCGGAGGAAAGATCTACGAGATC 1602
Qy 41 TyrLeuThrLeuHisLysProGluaspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 1603 TACCTCACATGCAACAGCCAGACGCTGAGGTTGCCCTAGCTGGCTGTTCAGACCCCTG 1662
Qy 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValileLeu 80
Db 1663 CTGAGTCAGTCGTTAGCTGTGGGCCCCCAGGAGTCCCTGCTCACC CGGCGCAGTCATCCTT 1722
Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db 1723 GCAATGGACCACTGTGGAGAGCCAGCCCTGCACAGCTGGAGTCTGGGCTCAAAAAGCAG 1782
Qy 101 SerCysGluGly 104
Db 1783 TCCTGCGAGGGC 1794
RESULT 12
US-10-296-115-365
; Sequence 365, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: HySeq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 365
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-365
Alignment Scores:
Pred. No.: 4,5e-59 Length: 1321
Score: 503.00 Matches: 103
Percent Similarity: 95.37% Conservative: 0
Best Local Similarity: 95.37% Mismatches: 1
Query Match: 89.98% Indels: 4
DB: 18 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x US-10-296-115-365 (1-1321)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
Db 94 ACCAGCAATGAGCTATGGACCTTCAACTTCCTCGGGGGCCGCTGATGATCCCTAAT 153
Qy 21 ThrGlyileSerLeuLeuileProAspAlaileProArgGlyLysileTyrGluile 40
Db 154 ACAGGAATCAGCTCTCTATACCCCGCAGATGCCATACCCCGAGGAAAGATCTATGAGATC 213
Qy 41 TyrLeuThrLeuHisLysProGluaspValArgLeuProLeuAlaGlyCysGlnThrLeu 60

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Db 214 TACCTCAGCTGCACAGCGGAGAGCTGAGGTGGCCCTAGCTGAGCTGCAGCCCTG 273
Qy 61 LeuSerProLeValSerCysGlyProPro-GlyValLeuLeuThrArgProValIleLe 80
Db 274 CTGAGTCCCATCGTTAGCTGTGGACCCCTCTGGCGTCTCTGCTTACCGCGCAGTCATCCT 333
Qy 80 u-AlaMetAspHisCys-GlyGluProSerProAspSerTrp-SerLeuArgLeuIleGly 99
Db 334 GGGGTATGGACCATCTGTGGGGAGCCAGCCCTGCACAGCTGGAGCCTGGCCCTCAAAAA 393
Qy 99 sGlnSerCysGluGly 104
Db 394 GCAGTCTGTCGAGGGC 409

RESULT 13
US-09-764-861-62/c
; Sequence 62, Application US/09764861
; Publication No. US20020086811A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204
; CURRENT APPLICATION NUMBER: US/09/764,861
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 9582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-861-62

Alignment Scores:
Pred. No.: 8.61e-43 Length: 9582
Score: 393.50 Matches: 83
Percent Similarity: 49.40% Conservative: 0
Best Local Similarity: 49.40% Mismatches: 0
Query Match: 70.39% Indels: 85
DB: 9 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-764-861-62 (1-9582)
Qy 22 GlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyr 41
Db 3709 GGAATCAGCTCTCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGATCTAC 3650
Qy 42 LeuThrLeuHisLysProGluAspVal----- 50
Db 3649 CTCACGCTGCACAGCGGAGAGAGCTGAGGTGTGGCCGCGGGCCCTGTTGCCGGGGTGG 3590
Qy 50 ----- 50
Db 3589 GAGGACCTGCTGCTGCTTCCGTTCCAGGAAGCCCTGCCACCCACTGTTGTGCC 3530
Qy 50 ----- 50
Db 3529 TGGCCCGAGCGCGGGGGAAGAGCTGTGCTTAAGCCCAAGCTGCTGCAGCCCAAG 3470
Qy 50 ----- 50
Db 3469 CCCCTGGCCCTGGATGCTGCTGCCCTTGGCCTAGCCCTCAGAGCCAGGATGG 3410
Qy 51 -----ArgLeuProLeuAlaGly 56
Db 3409 GCCACTGACACTTTTCCCTCCCAACCCATATTTCCCACTTGAGGTTGCCCTAGCTGGC 3350
Qy 57 CysGlnThrLeuLeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArg 76
Db 3349 TGTACAGACCTGCTGAGTCCCATCTGATGTGAGACCCCTCTGGGCTCTCTCACCCGG 3290
Qy 77 ProValIleLeuAlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArg 96
Db 3289 CCAGTCTCTCTGGCTATGGACCACTGTGGGAGGCCAGCCCTGCAGCTGGAGCTGGCC 3230
Qy 97 LeuIleLysGlnSerCysGluGly 104
Db 3229 CTCAAAAAGCAGTCTGTCGAGGGC 3206

RESULT 15
```

```
Db 3289 CCAGTCTCTCTGGCTATGGACCACTGTGGGAGGCCAGCCCTGCAGCTGGAGCTGGCC 3230
Qy 97 LeuIleLysGlnSerCysGluGly 104
Db 3229 CTCAAAAAGCAGTCTGTCGAGGGC 3206

RESULT 14
US-09-764-861-62/c
; Sequence 62, Application US/09764861
; Publication No. US20030171252A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204
; CURRENT APPLICATION NUMBER: US/09/764,861
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 9582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-861-62

Alignment Scores:
Pred. No.: 8.61e-43 Length: 9582
Score: 393.50 Matches: 83
Percent Similarity: 49.40% Conservative: 0
Best Local Similarity: 49.40% Mismatches: 0
Query Match: 70.39% Indels: 85
DB: 10 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-09-764-861-62 (1-9582)
Qy 22 GlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyr 41
Db 3709 GGAATCAGCTCTCTCATCCCCCAGATGCCATACCCCGAGGGAAGATCTATGATCTAC 3650
Qy 42 LeuThrLeuHisLysProGluAspVal----- 50
Db 3649 CTCACGCTGCACAGCGGAGAGAGCTGAGGTGTGGCCGCGGGCCCTGTTGCCGGGGTGG 3590
Qy 50 ----- 50
Db 3589 GAGGACCTGCTGCTGCTTCCGTTCCAGGAAGCCCTGCCACCCACTGTTGTGCC 3530
Qy 50 ----- 50
Db 3529 TGGCCCGAGCGCGGGGGAAGAGCTGTGCTTAAGCCCAAGCTGCTGCAGCCCAAG 3470
Qy 50 ----- 50
Db 3469 CCCCTGGCCCTGGATGCTGCTGCCCTTGGCCTAGCCCTCAGAGCCAGGATGG 3410
Qy 51 -----ArgLeuProLeuAlaGly 56
Db 3409 GCCACTGACACTTTTCCCTCCCAACCCATATTTCCCACTTGAGGTTGCCCTAGCTGGC 3350
Qy 57 CysGlnThrLeuLeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArg 76
Db 3349 TGTACAGACCTGCTGAGTCCCATCTGATGTGAGACCCCTCTGGGCTCTCTCACCCGG 3290
Qy 77 ProValIleLeuAlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArg 96
Db 3289 CCAGTCTCTCTGGCTATGGACCACTGTGGGAGGCCAGCCCTGCAGCTGGAGCTGGCC 3230
Qy 97 LeuIleLysGlnSerCysGluGly 104
Db 3229 CTCAAAAAGCAGTCTGTCGAGGGC 3206

RESULT 15
```

US-10-115-928-62/c
; Sequence 62, Application US/10115928
; Publication No. US20030092615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT204CI
; CURRENT APPLICATION NUMBER: US/10/115,928
; CURRENT FILING DATE: 2002-04-05
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 9582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-115-928-62

Alignment Scores:
Pred. No.: 8,61e-43 Length: 9582
Score: 393.50 Matches: 83
Percent Similarity: 49.40% Conservative: 0
Best Local Similarity: 49.40% Mismatches: 0
Query Match: 70.39% Indels: 85
DB: 14 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x US-10-115-928-62 (1-9582)

Qy	22	GlytSerLeuLeuLeuProProaspAlaIleProArgGlyValIleTyrCluIleTyr	41
Db	3709	GAAATCAGCCCTCTCATCCCCCAGATACCCCGAGGAAGATCTATGAGATCTAC	3650
Qy	42	LeuThrLeuHisLysProGluAspVal	50
Db	3649	CTCAGCTGCACAAAGCCGAGAGACCTGAGTGTGCGCGGGCCCTGTTCGGGGGTGG	3590
Qy	50	-----	50
Db	3589	GAGGACCTGCTGCTGCTTGGTTCGCCAGGAAGCCCTTGCCACCACCTGTTGTGCC	3530
Qy	50	-----	50
Db	3529	TGGCCCGAGCGCGCGGGGAAAGAGCTGTGCTAAGCCCAAGCTGCTGAGCCCAAG	3470
Qy	50	-----	50
Db	3469	CCCCCGCCCTGGGATGCTGCTGCCCTGGCCCTAGCCCTCAGGACCCAGGATGG	3410
Qy	51	-----ArgLeuProLeuAlaGly	56
Db	3409	GCCACTGACACCTTTCCCTCCACCACCATATTTCCCACTTGAGGTTGCCCTAGCTGGC	3350
Qy	57	CysGlnThrLeuLeuSerProIleValSerCysGlyProGlyValLeuLeuThrArg	76
Db	3349	TGTACAGCCCTGCTGAGTCCCATCTAGCTGTGAGCCCTTGGCGTCTGCTACCCGG	3290
Qy	77	ProValIleLeuAlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArg	96
Db	3289	CCAGTCATCTCTGCTATGACCACCTGTGGGAGCCAGCCCTGACAGCTGGAGCTGGGC	3230
Qy	97	LeuLysLysGlnSerCysGluGly	104
Db	3229	CTCAAAAGCAGTCGTGCGAGGCG	3206

Search completed: September 9, 2005, 18:52:38
Job time : 1049.83 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 22:38:37 ; Search time 3422.83 Seconds
(without alignments)
1156.553 Million cell updates/sec

Title: US-10-624-932C-2_COPY_495_598
Perfect score: 559
Sequence: 1 TSNMTYGTNFGRLMPN.....CCEPSPDSWLRLLKQSCG 104

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlh
-O=/csm2.1/USPTO spool h/US10624932/runat_08092005_161706_15792/app_query.fasta_1.1386
-DB=EST -OPT=fastap -SUFFIX=1st -MINMATCH=0.1 -LOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hnc:*
4: gb_est3:*
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7: gb_est6:*
8: gb_gssi:*
9: gb_gssi2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	ID	Description
1	559	100.0	788	1	AI951556
2	548	98.0	678	6	CAV49784
3	515	92.1	399	7	H43716
4	502	89.8	756	5	BUG12387
5	464	83.0	859	2	BF311896
6	460	82.3	382	7	R89529
7	397.5	71.1	934	2	BF311804
8	374	66.9	604	2	BE314370
9	354.5	63.4	815	7	CK140529

10	348	62.3	506	7	CF173478
11	348	62.3	2791	9	AY406493
12	348	62.3	3790	3	AK031655
13	337	60.3	329	1	AL119797
14	337	60.3	2802	9	AY406491
15	324	58.0	2802	9	AY406492
16	315	56.4	323	5	BQ339379
17	309	55.3	842	5	EX744794
18	303	54.2	731	1	AJ729964
19	302	54.0	874	5	BQ689148
20	302	54.0	889	5	BQ691915
21	295	52.8	1147	5	BQ840446
22	287	51.3	432	5	BQ339228
23	287	51.3	481	2	BF775467
24	287	51.3	537	2	BF073665
25	287	51.3	745	7	CK835492
26	287	51.3	770	1	AU127790
27	287	51.3	986	5	BQ709159
28	287	51.3	2532	9	AY411747
29	281	50.3	798	6	CB592227
30	277	49.6	810	6	CA511645
31	274	49.0	673	5	BU611727
32	274	49.0	816	7	CN527193
33	274	49.0	2532	9	AY411749
34	274	49.0	3866	3	AK018177
35	269	48.1	348	4	BF950493
36	268	47.9	524	2	AW654577
37	252	45.1	352	7	CN219416
38	221	39.5	2532	9	AY411748
39	220	39.4	343	4	BF946952
40	212	37.9	860	2	BF312306
41	207	37.0	939	4	BG331653
42	195.5	35.0	990	5	BQ707104
43	193	34.5	735	7	CN441440
44	192	34.3	464	2	AW629051
45	192	34.3	537	5	EX094642

ALIGNMENTS

RESULT 1
AI951556
LOCUS
DEFINITION
AI951556 788 bp mRNA linear EST 09-MAR-2000
wv36f04.x1 NCI CGAP Ov18 Homo sapiens cDNA clone IMAGE:2531647 3',
similar to TR:O08721 O08721 TRANSMEMBRANE RECEPTOR UNC5H1. ;, mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AI951556.1 GI:5743866
EST.
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 788)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 1125 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 446.
Location/Qualifiers
1. .788

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clonename="IMAGE:2531647"
/tissue_type="fibrotheoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI_CGAP_Ov18"
/notes="Organ: ovary; Vector: p77T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; let strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTCGGAGCGCGGACATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p77T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
```

ORIGIN

```

Alignment Scores:
Pred. No.:      2.57e-50      Length:      788
Score:          559.00      Matches:    104
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:    0
DB:              1          Gaps:      0
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US-10-624-932C-2_COPY_495_598 (1-104) x AT951556 (1-788)

```

Qy      1  ThrSerAsnMetThrTyrGlyThrPheAsnPhelLeuGlyGlyArgLeuMetIleProAsn 20
Db      60  ACCAGCACATGACCTATGGACCTTCACTTCCTCGGGGCGGCTGATGATCCCTAAT 119
Qy      21  ThrGlyIleSerLeuLeuProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db      120  ACAGGAATCAGCTCTCATCCCCCAGATGCATACCCGAGGGAAGATCTATGAGATC 179
Qy      41  TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db      180  TACCTTCACGCTGCACAAACCGGAGACGTAGGTGGCCCTAGCTGGCTGTGCAGACCTG 239
Qy      61  LeuSerProIleValSerCysGlyProGlyValLeuLeuThrArgProValIleLeu 80
Db      240  CTGAGTCCCATCGTTAGCTGTGGACCCCTCGCGTCTGCTACCCGCGCAGTCATCTG 299
Qy      81  AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db      300  GCTATGGACCACTGTGGGAGCCAGCCCTGACAGCTGGAGCTCGCGCTCAAAAAGCAG 359
Qy      101  SerCysGluGly 104
Db      360  TCGTCGAGGGG 371
```

RESULT 2

```

CA749784
LOCUS      CA749784
DEFINITION UI-M-FD0-cdg-c-11-0-UI-r1 NIH_BMAP_F00 Mus musculus cDNA clone
IMAGE:6828324 5', mRNA sequence.
```

CA749784

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 678)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.
Location/Qualifiers

```

1. 678
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6828324"
/tissue_type="whole brain"
/dev stage="embryo 12.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_F00"
/notes="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; the library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
```

FEATURES

SOURCE

ORIGIN

```

Alignment Scores:
Pred. No.:      3.34e-49      Length:      678
Score:          548.00      Matches:    102
Percent Similarity: 98.08%      Conservative: 0
Best Local Similarity: 98.08%      Mismatches: 2
Query Match:      98.03%      Indels:    0
DB:              6          Gaps:      0
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US-10-624-932C-2_COPY_495_598 (1-104) x CA749784 (1-678)

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Qy      1  ThrSerAsnMetThrTyrGlyThrPheAsnPhelLeuGlyGlyArgLeuMetIleProAsn 20
Db      226  ACCAGCAATCGCTTATGGACCTTCACTTCCTCGGGGCGGCTGATGATCCCTAAC 285
Qy      21  ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyrGluIle 40
Db      286  ACAGGAATCAGCTCTCTCATCCCCCGAGCGCCATCCCCGAGGAAGAATCTACGAGATC 345
Qy      41  TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db      346  TACCTTCATCTGCAACAGCCAGAGACGTAGGTGGCCCTAGCTGGCTGTGCAGACCTG 405
Qy      61  LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
Db      406  CTGAGTCTCTATCGTTAGCTGTGGGCCCCAGGAGTCTCTGCTACCCGCGCAGTCATCTT 465
Qy      81  AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGln 100
Db      466  GCCATGGACCACTGTGGGAGGCCAGTCGCCAGACAGCTGGAGCCTGCGCCTCAAAAAGCAG 525
Qy      101  SerCysGluGly 104
Db      526  TCGTGTGAGGG 537
```

RESULT 3

H43716

LOCUS

DEFINITION

yo80g05.81 Soares adult brain N2b4HB55y Homo sapiens cDNA clone

399 bp

mRNA

linear

EST 31-JUL-1995

Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20

(BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:
 Pred. No.: 3.78e-44 Length: 756
 Score: 502.00 Matches: 94
 Percent Similarity: 97.92% Conservative: 0
 Best Local Similarity: 97.92% Mismatches: 2
 Query Match: 89.80% Indels: 0
 DB: 5 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x BU612387 (1-756)

Qy 1 ThrSerAnMetThrTyTGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
 Db 467 ACCAGCAATGCGCTATGGACCTTCAACTTCCTCGGGGGCGGCTGATGATCCCTAAC 526
 Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyGluIle 40
 Db 527 ACAGGAATCAGCTCCTCATACCCCGGACGCCATCCCGGAGGAAGATCTACGAGATC 586
 Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrIle 60
 Db 587 TACCTCATCTGCAACAGCAGACAGCTGAGGTGCCCCCTAGCTGGCTGTCAGACCCCTG 646
 Qy 61 LeuSerProfileValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
 Db 647 CTGAGTCTATCGTTAGCTGTGGGCCCCCAGGAGTCTCTGCTCACCGGCCAGTCTCTT 706
 Qy 81 AlaMetAspHisCysGlyGluProSerProAspSerTrpSerLeuArg 96
 Db 707 GCCATGGACCACTCGGGGAGCCCGAGTCNCACAGCTGGAGCCTGCGC 754

RESULT 5
 BF311896
 LOCUS 601897733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126760 5',
 DEFINITION mRNA sequence.

ACCESSION BF311896

VERSION BF311896

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NIH-MGC <http://mhc.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: L101017 row: b column: 09

High quality sequence stop: 684.

Location/Qualifiers

FEATURES

source

1..859

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4126760"

/tissue_type="neuroblastoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_19"

/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 5.93e-40 Length: 859
 Score: 464.00 Matches: 95
 Percent Similarity: 92.38% Conservative: 2
 Best Local Similarity: 90.48% Mismatches: 7
 Query Match: 83.01% Indels: 2
 DB: 2 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x BF311896 (1-859)

Qy 1 ThrSerAnMetThrTyTGlyThrPheAsnPheLeuGlyGlyArgLeuMetIleProAsn 20
 Db 412 ACCAGCAATGCGCTATGGACCTTCAACTTCCTCGGGGGCGGCTGATGATCCCTAAT 471
 Qy 21 ThrGlyIleSerLeuLeuIleProProAspAlaIleProArgGlyLysIleTyGluIle 40
 Db 472 ACAGGAATCAGCTCCTCATACCCCGGACGCCATACCCGAGGAAGATCTATGAGATC 531
 Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrIle 60
 Db 532 TACCTCATCTGCAACAGCAGACAGCTGAGGTGCCCCCTAGCTGGCTGTCAGACCCCTG 591
 Qy 61 LeuSerProfileValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeu 80
 Db 592 CTGAGTCTCATCGTTAGCTGTGGACCCCTGCGCTCTGCTCACCGGCCAGTCTCTCTG 651
 Qy 81 AlaMet-AspHisCysGlyGluProSerProAspSerTrpSerLeuArgLeuLysGly 100
 Db 652 GCTATGGGACCACTGTGCGGGAGCCAGCTGACAGCTTGGAGCCTGGGC-CTCAAAAAGCA 710
 Qy 100 nSerCysGluGly 104
 Db 711 GCGCTGCTAAGGG 723

RESULT 6

R89529

LOCUS

DEFINITION

Ym97d12.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone

IMAGE:166871 3', mRNA sequence.

ACCESSION R89529

VERSION R89529.1 GI:954356

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 382)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Woldmann,P. and

Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1642

High quality sequence stops: 298 Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: polyT not found

Insert Length: 1642 Std Error: 0.00

Seq primer: Promega -21m13
High quality sequence stop: 298.

FEATURES

Location/Qualifiers
1..382
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:587566"
/db_xref="taxon:9606"
/clone="IMAGE:166871"
/sex="Male"
/dev_stage="55-year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2B4HB55Y"
/note="Organ: brain; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATCTGAGTGGGAGCGCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M. Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

US-10-624-932C-2_COPY_495_598 (1-104) x R89529 (1-382)

ORIGIN

Alignment Scores:
Pred. No.: 5,958-40 Length: 382
Score: 460.00 Matches: 92
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 82.29% Indels: 3
DB: 7 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x R89529 (1-382)

QY 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetileProAsn 20
DB 98 ACCAGCAACATGACCTATGGGACCTTCAACTTCTCGGGGCGGCTGATGATCCCTAAT 157
QY 21 ThrGlyIleSerLeuLeuLeuLeuProProAspAlaIleProArgGlyIleTyrGluile 40
DB 158 ACAGGAATCAGCTCTCTATCCCTCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 217
QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
DB 218 TACCTCAGCTGCACACGCGGAGAGAGCTGAGGTGGCCCTAGCTGGCTGCAGACCTG 277
QY 61 LeuSerProIleValSerCysGlyProPro-GlyValLeuLeuThrArgProValileLe 80
DB 278 CTGAGTCCCATCGTTAGCTGTGGACCCCTCGGGCGTCTGCTTACCCGCGCAGTCATCCT 337
QY 80 u-AlaMetAspHisCys-GlyGluProSerProAspSerTTP 93
DB 338 GGGGTATGAGACCACTGTGGGGAGCCAGCCCTGACAGCTGG 379

RESULT 7
BF311804
LOCUS 601897316F1 NTH_MGC_19 Homo sapiens cDNA clone IMAGE:4126706 5',
DEFINITION mRNA sequence.
ACCESSION BF311804
VERSION BF311804.1 GI:11259566
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1. (bases 1 to 934)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW1016 row: p column: 03
High quality sequence stop: 707.

FEATURES

source

1..934
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4126706"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 1,1e-32 Length: 934
Score: 397.50 Matches: 89
Percent Similarity: 85.71% Conservative: 1
Best Local Similarity: 84.76% Mismatches: 14
Query Match: 71.11% Indels: 4
DB: 2 Gaps: 1

US-10-624-932C-2_COPY_495_598 (1-104) x BF311804 (1-934)

QY 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyGlyArgLeuMetileProAsn 20
DB 414 ACCAGCAACATGACCTATGGGACCTTCAACTTCTCGGGGCGGCTGATGATCCCTAAT 473
QY 21 ThrGlyIleSerLeuLeuLeuLeuProProAspAlaIleProArgGlyIleTyrGluile 40
DB 474 ACAGGAATCAG-CTCTCATCCCTCCAGATGCCATACCCCGAGGGAAGATCTATGAGATC 532
QY 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
DB 533 TACCTCAGCTGCACACGCGGAGAGAGCTGAGGTGGCCCTAGCTGGCTGCAGACCTG 591
QY 61 LeuSerProIleValSerCysGlyProProGlyValLeuLeuThrArgProValileLeu 80
DB 592 CTGAGTCCCATCGTTAGCTGTGGACCCCTCGGGCGTCTGCTTACCCGCGCAGTCATCCT 651
QY 81 Ala---MetAspHisCysGlyGluProSerProAspSerTTPSerLeuArgLeuLys 99
DB 652 GGCTAATGAGCCCACTGTGGGGAAGC-CAGCCTGACATGGAGCTTGGGCTCAAAAAGG 710
QY 100 GlnSerCysGluGly 104
DB 711 AGTCGTGCGAGGGC 725

RESULT 8

BE314370

LOCUS

DEFINITION

BE314370 60147261F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3162710 5',
linear EST 26-OCT-2000

```

mRNA sequence.
ACCESSION BE314370
VERSION BE314370.1 GI:9135413
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L10M122 row: 1 column: 15
High quality sequence stop: 601.
Location/Qualifiers
FEATURES
source
1. .604
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3162710"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 19"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 2,298-30 Length: 604
Score: 374.00 Matches: 70
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.91% Indels: 0
DB: 2 Gaps: 0
US-10-624-932C-2_COPY_495_598 (1-104) x BE314370 (1-604)
Qy 1 ThrSerAsnMetThrTyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsn 20
Db 395 ACCAGCAACATGACCATATGGACCTTCAACTTCTCGGGGCGCGCTGATCCCTAAT 454
Qy 21 ThrGlyIleSerLeuLeuProAspAlaIleProArgGlyValIleTyrGluIle 40
Db 455 ACAGGAATCAGCCTCTCATCCCCCAGATGCCATACCCGAGGAGATCTATGAGATC 514
Qy 41 TyrLeuThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeu 60
Db 515 TACCTCAGCTGCACACCGAGAGCTGAGGTTCCTAGCTGGCTGTGACAGCCCTG 574
Qy 61 LeuSerProIleValSerCysGlyProPro 70
Db 575 CTGATGCCATCGTTAGCTGTGGACCCCGC 604
RESULT 9
CK140529 815 bp mRNA linear EST 03-DEC-2003
LOCUS AGNCOURT_16886288 NCI_CGAP_ZEMB3 Danio rerio cDNA clone
IMAGE:7058133 5', mRNA sequence.
ACCESSION CK140529
mRNA sequence.
VERSION CK140529.1 GI:38651455
KEYWORDS EST.
SOURCE
ORGANISM Danio rerio (zebrafish)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
JOURNAL Cypriniformes; Cyprinidae; Danio.
COMMENT 1 (bases 1 to 815)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Chi-Bin Chien
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10M14841 row: f column: 19
High quality sequence start: 5
High quality sequence stop: 746.
Location/Qualifiers
FEATURES
source
1. .815
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:7058133"
/tissue_type="embryo"
/lab_host="NCI_CGAP_ZEMB3"
/clone_lib="NCI_CGAP_ZEMB3"
/note="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.1 Kb. Constructed by J. Wang (Research Genetics,
Invitrogen Corp) from tissue donated by L. Zon (Harvard
University). Note: this is a NCI_CGAP Library."
ORIGIN
Alignment Scores:
Pred. No.: 4,34e-28 Length: 815
Score: 354.50 Matches: 67
Percent Similarity: 85.71% Conservative: 11
Best Local Similarity: 73.63% Mismatches: 12
Query Match: 63.42% Indels: 2
DB: 7 Gaps: 1
US-10-624-932C-2_COPY_495_598 (1-104) x CK140529 (1-815)
Qy 3 AsnMetThrTyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGly 22
Db 527 AACACCTCGTACGCACTTCAACTTCTCGGGCGAGCGACTGAGCTGCCACACGGA 586
Qy 23 IleSerLeuLeuIleProAspAlaIleProArgGlyValIleTyrGluIleTyrLeu 42
Db 587 ATCAGCTGTCTATCCCGCAGAGCCATTCCTCCAGAGGAGAGATTACGAGATTACCTC 646
Qy 43 ThrLeuHisLysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSer 62
Db 647 ACTATTGAGAGAGAGAGAGATGAGGCTCCGCTGGGGGCTGTCAGAGCGTCTGAGC 706
Qy 63 ProIleValSerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMet 82
Db 707 CCCGTGTGAGCTGCGGACCGCCGCGCTCATGTCTCANC CGCGCTCATCTCTG---CAT 763
Qy 83 AspHisCysGlyGluProSerProAspSerTrp 93
Db 764 GGACACTGCTCAGATGCTGCTGCTG-GAGAACTGG 795
RESULT 10

```

CF173478
 LOCUS B0924C04-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
 DEFINITION musculus cDNA clone NIA:B0924C04 IMAGE:30474555 5', mRNA sequence.
 ACCESSION CF173478
 VERSION CF173478.1 GI:33283027
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Piao, Y., Ko, N.Y., Lim, M.K. and Ko, M.S.H.
 Construction of long-transcript enriched cDNA libraries from
 submicrogram amounts of total RNAs by a universal PCR amplification
 method
 Genome Res. 11 (9), 1553-1558 (2001)
 21429098
 11544199
 CONTACT: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: B0924 row: C column: 04
 Seq primer: M13 Reverse
 High quality sequence stop: 506
 POLYA=No.
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 source
 1..506
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="niaEST:B0924C04-5"
 /db_xref="taxon:10090"
 /clone="NIA:B0924C04 IMAGE:30474555"
 /dev_stage="Unfertilized Egg"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long 1)"
 /note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). (PMID: 11544199)). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen): 5'-pGACTAGTTCTAGATCGGCGCGCCCTTTTTTTTTT-3', treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LL-SalI, purified by phenol/chloroform, and cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."

ORIGIN

Alignment Scores:
 Pred. No.: 1.23e-27 Length: 506
 Score: 348.00 Matches: 58
 Percent Similarity: 81.82% Conservative: 23
 Best Local Similarity: 58.59% Mismatches: 18
 Query Match: 62.25% Indels: 0
 Gaps: 0
 DB:

US-10-624-932C-2_COPY_495_598 (1-104) x CF173478 (1-506)
 QY 6 TyrGlyThrPheAspPheLeuGlyGlyArgLeuMetIleProAsnThrGlyIleSerLeu 25
 ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 186 TTTGGTACTTCAACTCTCTTGGGGGTCACTCATCATCTCTTAATTCAGGAGTAGCTTG 245
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 26 LeulleProProAspAlaIleProArgGlyIleTyrGluIleTyrLeuThrLeuHis 45
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 246 CTGATTCCCGTGGGGCCATTCTCAGGGAGAGTCTATGAATGTATGTGACTGTACAC 305
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 46 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 65
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 306 AGGAAGAAAATATAGAGCCCCCATCTGGAAGACTCTCAGACCTACTTACCCCTGTGGTG 365
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 66 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 85
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 366 AGCTGTGGGCTCTCTGGAGCTCTGCTGACCCGCCCTGTCTATCTCTGCATCTGT 425
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 86 GlyGluProSerProAspSerTyrSerLeuArgLeuLysGlnSerCysGluGly 104
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 426 CGAGACCCAGCAGCAGGAGTGGAGATCCAGCTCAAAAACCCAGGCAGTCAGGGA 482
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 RESULT 11
 LOCUS AY406493 2791 bp DNA linear GSS 15-DEC-2003
 DEFINITION Mus musculus UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY406493
 VERSION AY406493.1 GI:39762467
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 JOURNAL PUBMED 14671302
 REFERENCE 2 (bases 1 to 2791)
 AUTHORS Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES
 source
 1..2791
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 <1..>2791
 /gene="UNC5C"
 /locus_tag="HCW2575"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1e-26 Length: 2791
 Score: 348.00 Matches: 58
 Percent Similarity: 81.82% Conservative: 23
 Best Local Similarity: 58.59% Mismatches: 18
 Query Match: 62.25% Indels: 0
 Gaps: 0
 DB: US-10-624-932C-2_COPY_495_598 (1-104) x AY406493 (1-2791)

Qy 6 TyrGlyThrPheAenPheLeuGlyGlyArgLeuMetIleProAenThrGlyIleSerIeu 25
 Db 1592 TTTGGTACCTTCAACTCTCTTTGGGGGTCACTCATCATCTCTTAATTCAGGAGTAAAGCTTG 1651

Qy 26 LeuIleProProAspAlaIleProArgGlyLysIleTyrGluIleTyrLeuThrLeuHis 45
 Db 1652 CTGATTCCTCCGCTGGGGCCATTCCTCAGGGGAGAGTCTATGAATATGATGACATGTACAC 1711

Qy 46 LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 65
 Db 1712 AGGAAGAAATATGAGGCCCCCATGGAAGACTCTCAGACCTACTTACCCCTGTGGTG 1771

Qy 66 SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 85
 Db 1772 AGCTGTGGGCTCTCGAGGCTCTGCTGACCGCCCTGTCATCCCTACTCTGCATCACTGT 1831

Qy 86 GlyGluProSerProAspSerTrpSerLeuArgLeuLysLysGlnSerCysGluGly 104
 Db 1832 GCAGACCCAGCAGGAGCTGGAGATCCAGCTCAAAAACAGGACGAGTCAGGGA 1888

RESULT 12
 LOCUS AK031655
 DEFINITION Mus musculus 3790 bp mRNA linear HTC 03-APR-2004
 enriched library, clone:6030473H24 product:unc5 homolog (C. elegans) 3, full insert sequence.

ACCESSION AK031655
 VERSION AK031655.1 GI:26327502
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis, (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 3790)
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuura, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/.

FEATURES
 source Location/Qualifiers
 1. 3790
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM DB:6030473H24"
 /db_xref="taxon:10090"
 /clone="6030473H24"
 /sex="male"
 /tissue_type="testis"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="13 days embryo"
 118..2970
 /note="unnamed protein product; putative unc5 homolog (C. elegans) 3 (MGD|GI:1095412, GB|NM_009472, evidence: BLASTN, 99%, match=464)"
 /codon_start=1
 /protein_id="BAC27495.1"
 /translation="MRKGLRATAARCGLGIGYLLQMLVLPALALLSASGTSAAQDDE FFHELPTFPDPPEPLPHFLIPEEAYIVKPKVNLCKASPATQIYFKCNSEWHQ KDHWDRVDETSGLIIVREVISIISROQVEELFGPDYWCQCVAMSGAGTKSKAVV TIADRLKTFEQLGKEVSLQEVLVLCQRPPEGI PVAEVELKNEDIIDPAEDRNFYI TDHNLIIKQARLSDTANYTCVAKNIIVAKKSTATIVIVYUNGWSTWTSVCNSRC GRGQKTRTCTNPAPLNGAGFCGQGVQKIACTTLCFVDRWTSWKNSTCGTECTH WDRRECTAPAPKNGKDCDGLVQLQSKNCTDGLCMQGFIPYISTEHRPONEYGFSSAP RDLLAVPDLTSAAMRGVVALHDVSDKIPMTNSPILDPPLNLKIKVNSSCAVT PODLAEFSSKLSPQMTQVSIILEALNLKQSLAROTDPSCTAFGTNSLGGHLIIPN SGVSLIIPAGALPQGRYEMVYVTHKENRPMEDSQTLITPVSQCPGALLTRPV ILTLHHCADPSTEDWKIQLKNQAVQGVQWEDVVVGEENFTTPCIIQDARACHLTEN LSTYALVGQSTTKAAAKRLKLAIFGLPCSSLSYIRVCLDDTQDALKVQLERQM GGQLEEPKALRFKGSIHNLRSIHDIHAHLSKJLAKYQEI PFYHWSGSQRNLHC TFTLERLSLNTVELVCKLCVROGEQIIFQNLCTVSEPTGIDLPILDPASTITVT GPASFSIPLPIROKLCSSLDAPOTRGHDWRMLAKHLNLYNFATKSSPTGTVILD WEAQNFDPDGNLSMLAVLEEMGRHETVTVLAABEQY"

ORIGIN
 Alignment Scores:
 Pred. No.: 1,46e-26 Length: 3790
 Score: 348.00 Matches: 58
 Percent Similarity: 81.82% Conservative: 23
 Best Local Similarity: 58.59% Mismatches: 18
 Query Match: 62.25% Indels: 0
 DB: 3 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x AK031655 (1-3790)

```

QY      6  TyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeu 25
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1771 TTTGGTACCTTCAACTCTCTTGGGGTCACTCATCTTCCATTCCTAATTCAGAGTAGCTTG 1830

QY      26  LeuIleProProAspAlaIleProArgGlyIleTyrGluIleTyrLeuThrLeuHis 45
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1831 CTGATTCCCGCTGGGGCCATTCTCAGGGGAGAGTCTATGAATGTATGATGCTGTACAC 1890

QY      46  LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 65
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1891 AGAAGAAGAAATATGAGGCCCTCATGGAAGACTCTCAGACCTACTTACCCCTGTGGTG 1950

QY      66  SerCysGlyProProGlyValLeuLeuThrArgProValIleLeuAlaMetAspHisCys 85
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1951 AGCTGTGGGCTCTGTGAGCTCTGTGACCCGCGCTGTCTCACTCTGCATCACTGT 2010

QY      86  GlyGluProSerProAspSerTrpSerLeuArgLeuLysGlnSerCysGluGly 104
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2011 GCAGACCCCGAGCAGGAGTCCAGATCCAGCTCAAAACACGAGCAGTGCAGGGA 2067

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RESULT 13

AL119797
LOCUS AL119797 329 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp761G1524 r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1524 5', mRNA sequence.
ACCESSION AL119797
VERSION AL119797.1 GI:5925696
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 329)
AUTHORS Bloeker,H., Boecher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Bloeker, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No si sequence available.
 This clone (DKFZp761G1524) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clones@rzpd.de.

FEATURES

source
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 /db_xref="taxon:9606"
 /clone="DKFZp761G1524"
 /tissue_type="amygdala"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="761 (synonym: hamy2)"
 /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

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 Score: 337.00 Matches: 55
 Percent Similarity: 79.80% Conservative: 24
 Best Local Similarity: 55.56% Mismatches: 20
 Query Match: 60.29% Indels: 0
 DB: 1 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x AL119797 (1-329)

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QY      6  TyrGlyThrPheAsnPheLeuGlyArgLeuMetIleProAsnThrGlyIleSerLeu 25
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Db      21  TTTGAGAGCTTCAACTCGCTGGAGGTCACTTATGTGTCCCAATTCAGAGTCAGCTTG 80

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Db      81  CTGATTCCCGCTGGGGCCATTCCCAAGGGAGAGTCTACGAATGTATGATGCTGTACAC 140

QY      46  LysProGluAspValArgLeuProLeuAlaGlyCysGlnThrLeuLeuSerProIleVal 65
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      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      201 AGCTGTGGGCCCCCAGGAGCTCTGCTCACCGCCCCGCTCGTCTCACTATGTCATGTC 260

QY      86  GlyGluProSerProAspSerTrpSerLeuArgLeuLysGlnSerCysGluGly 104
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      261 GCAGACCCCAATACCAGGAGCTGGAAATACTGCTCAAGAACCGAGCAGCAGGGA 317

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RESULT 14

AY406491
LOCUS AY406491 2802 bp DNA linear GSS 15-DEC-2003
DEFINITION Homo sapiens UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY406491
VERSION AY406491.1 GI:39762465
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2802)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2802)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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 /gene="UNC5C"
 /locus_tag="HCW2575"

ORIGIN

Alignment Scores:
 Pred. No.: 1.58e-25 Length: 2802
 Score: 337.00 Matches: 55
 Percent Similarity: 79.80% Conservative: 24
 Best Local Similarity: 55.56% Mismatches: 20
 Query Match: 60.29% Indels: 0
 DB: 9 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x AY406491 (1-2802)

Qy	6	Tyr-GlyThrPheAsnPhelLeuGlyArgLeuMetIleProAnthrGlyIleSerLeu	25
Dd	1603	TTTGGCAGCTTCAACTCGCTGGGAGGTTCACCTTATTGTTCCCAATTCCAGAGTCAGCTTG	1662
Qy	26	LeulleProProaspAlalleProAargGlyVysilleTyrgluiletyrCluiletyrLeuthrLeuHis	45
Dd	1663	CTGAATCCCCCTGGGGCCCATTTCCCAAGGAGAGTCTACAAATATGATGTATGCATGTACAC	1722
Qy	46	LvsProgluAspValargLeuProLeuAlaagLyCysglnThrLeuleuSerProIleVal	65
Dd	1723	AGAAAGAAATAATAGGCCACCACCGATGATCTCTCAGACATTTTGGACCTTGTGGT	1782
Qy	66	SerCyeglyProProglyValLeuLeuThArgrProValleLeuAlaMetAspHisCys	85
Dd	1783	AGCTGTGGGCCCCCAGGAGCTCTGCTCACCGCCAGTCGCTCCTCACTATGTCATCACTGTC	1842
Qy	86	GlyCluProSerProaspSerTrpSerLeuAargLeuLysglnSerCysGlugly	104
Dd	1843	GCAGACCCCAATACCGAGGACTGAAATAATGCTCAAGAACCAGGCAGCACAGGGA	1899

RESULT 15
AY406492

LOCUS
DEFINITION Pan troglodytes UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION AY406492

VERSION AY406492.1 GI:39762466

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 2802)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 2802)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
source Location/Qualifiers
1..2802
 /organisms="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
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 /gene="UNC5C"
 /locus_tag="HCM2575"

gene

ORIGIN

Alignment Scores:
Pred. No.: 4,07e-24 Length: 2802
Score: 324.00 Matches: 53
Percent Similarity: 77.78% Conservative: 24
Best Local Similarity: 53.54% Mismatches: 22
Query Match: 57.96% Indels: 0
DB: 9 Gaps: 0

US-10-624-932C-2_COPY_495_598 (1-104) x AY406492 (1-2802)

Qy	6	Tyr-glyThrPheAsnPhelLeuGlyArgLeuMetIleProAnthrGlyIleSerLeu	25
Dd	:	:::::	:::::

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 23:47:02 ; Search time 3365.92 Seconds
(without alignments)
1166.064 Million cell updates/sec

Title: US-10-624-932C-2_COPY_817_897

Perfect score: 423
Sequence: 1 QKITSLLPPCRGDMRTL.....AAVAGLGQPDAGLFTVSEAE 81

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO spool_h/US10624932/runat_08092005_161705_15773/app_query.fasta_1.1386
-DB=GenEmbl -QFMT=fastap -SURFIX=arg -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10624932@cgn 1 1 7509 @runat_08092005_161705_15773 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	423	100.0	2688	9 BC009333	Homo sapi
2	423	100.0	2697	6 AX451652	Sequence
3	423	100.0	2752	6 AX449572	Sequence
4	423	100.0	2784	6 CQ730306	Sequence

5	423	100.0	2881	6 AX527916	Sequence
6	423	100.0	3580	6 AX367094	Sequence
7	423	100.0	9700	6 AX054976	Sequence
8	410	96.9	2697	6 AX268596	Sequence
9	410	96.9	2697	10 RN087305	Sequence
10	410	96.9	3014	6 BD057524	Netrin re
11	410	96.9	3844	10 BC058084	Mus muscu
12	410	96.9	3992	10 MM0487852	Mus muscu
13	410	96.9	4294	10 AK122575	Netrin re
14	376	88.9	1787	6 BD057525	Netrin re
15	359.5	85.0	171419	2 AC135142	Rattus no
16	359.5	85.0	231407	2 AC135952	Rattus no
17	357.5	84.5	6495	9 AB075856	Homo sapi
18	357.5	84.5	6522	6 BD186447	Novel gen
19	357.5	84.5	121282	9 AC027318	Homo sapi
20	357.5	84.5	166534	2 AC034209	Homo sapi
21	352.5	83.3	242128	2 AC123700	Mus muscu
22	351.5	83.1	168168	2 AC012283	Homo sapi
23	305	72.1	276	6 AX451658	Sequence
24	304	71.9	341	6 CQ460895	Sequence
25	222	52.5	1575	6 AX054890	Sequence
26	221	52.2	1393	6 AX054886	Sequence
27	221	52.2	1438	6 AX054888	Sequence
28	221	52.2	2013	6 CQ729046	Sequence
29	221	52.2	2612	6 CQ881064	Sequence
30	221	52.2	2780	6 CQ881054	Sequence
31	221	52.2	2986	6 CQ881052	Sequence
32	221	52.2	3646	6 CQ881060	Sequence
33	221	52.2	3646	9 AF055634	Homo sapi
34	221	52.2	9299	10 MMU72634	Mus muscu
35	221	52.2	9328	10 AB118026	Rattus no
36	217	51.3	2962	5 AY187310	Gallus ga
37	201	47.5	3672	10 BC048162	Mus muscu
38	201	47.5	3672	10 BC057560	Mus muscu
39	201	47.5	3788	10 MMU487853	Mus muscu
40	199	47.0	2832	5 AX099459	Xenopus l
41	198	46.8	2831	6 BD057526	Netrin re
42	198	46.8	2838	10 RN087306	Rattus norv
43	191	45.2	1948	6 BD159676	Primer fo
44	191	45.2	1948	6 AX882354	Sequence
45	191	45.2	1948	9 AK022859	Homo sapi

ALIGNMENTS

RESULT 1	BC009333	2688 bp	mrna	linear	PRI_25-MAR-2004
LOCUS	BC009333				
DEFINITION	Homo sapiens unc-5 homolog A (C. elegans), partial cds.				
ACCESSION	BC009333				
VERSION	BC009333.2				
KEYWORDS	GI:40226527				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 2688)				
	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toehiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,				

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krayninski, M.I., Skaleka U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 2688)
Strausberg, R.
Direct Submission
Submitted (12-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Dec 19, 2003 this sequence version replaced gi:14424611.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisec.nih.gov/>
Contact: nisc_mgc@hgrl.nih.gov
Ahter, N., Ayle, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brookes, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Scantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 26 Row: 9 Column: 22.
Location/Qualifiers
1..2688
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413..724
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misc_feature

/note="ZUS; Region: Domain present in ZO-1 and Uncs-like netrin receptors"
/db_xref="CDD:smart00218"
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/note="DEATH; Region: DEATH domain, found in proteins involved in cell death (apoptosis). Alpha-helical domain present in a variety of proteins with apoptotic functions. Some (but not all) of these domains form homotypic and heterotypic dimers"
/db_xref="CDD:smart00005"

misc_feature

Alignment Scores:
Pred. No.: 1.39e-41 Length: 2688
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x BC009333 (1-2688)
Qy 1 GlnYsilelleSerSerLeuAspProCySArgArgGlyAlaAspTrpArgThrLeu 20
Db 1379 CAGAAGATAATTTCCAGCTGGACCCACCTGTAGGCGGGTGCAGCTGCGGACTCTG 1438
Qy 21 AlaGlnYsleuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1439 GCCCAGAAATCCACCTGGACGACATCTCAGCTTCTTTGGCTCCAGCCCGCCACA 1498
Qy 41 AlaMetIleLeuAnLeuTtpGluAlaArgHisPheProAnGlyVasLeuSerGlnLeu 60
Db 1499 GCCATGATCTCACTTGTGGAGCGCGGCACCTTCCCACGCGCACTCAGCCAGCTG 1558
Qy 61 AlalaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 1559 GCTCAGCAGTGGCTGGACTGGGCGCAGCCAGCAGCTGGCTTTCACAGTGTGAGGCT 1618
Qy 81 Glu 81
Db 1619 GAG 1621
RESULT 2
AX451652
LOCUS AX451652 2697 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1 from Patent WO0233080.
ACCESSION AX451652
VERSION AX451652.1 GI:21698587
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Koehler, R.H.
TITLE Regulation of human netrin binding membrane receptor unc5h-1
JOURNAL Patent: WO 0233080-A 1 25-APR-2002;
Bayer Aktiengesellschaft (DE)
FEATURES
source
1..2697
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.39e-41 Length: 2697
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x AX451652 (1-2697)

QY 1 GlnLysIleSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
|||||
Db 2449 CAGAAGATAATTTCCAGCTGTGACCCACCTGTAGCGGGTGGCGACTGCGGACTCTG 2508

QY 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
|||||
Db 2509 GCCCAGAAATCCACCTGACAGCATCTCAGCTTTTGTGCTCCCAAGCCAGCCGCCACA 2568

QY 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
|||||
Db 2569 GCCATGATCCTCAACCTGTGGAGGCGGGCACTTCCCAAGCGCAACTCAGCCAGCTG 2628

QY 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
|||||
Db 2629 GCTGACAGAGTGGCTGGACTGGCCAGCAGACGCTGGCTTTTACAGTGTGCGAGGCT 2689

QY 81 Glu 81
|||||
Db 2689 GAG 2691

RESULT 3
LOCUS AX449572 2752 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1 from Patent WO210216.
ACCESSION AX449572
VERSION AX449572.1 GI:21698195

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Padigar, M., Mezes, P., Mishra, V., Burgess, C., Casman, S.,
Grosse, W.M., Alsobrook, J.P., Lepley, D.M., Gerlach, V.L.,
Macdougall, J.R. and Smithson, G.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0210216-A 1 07-FEB-2002;
Curagen Corporation (US)

FEATURES
source
1..2752
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.42e-41 Length: 2752
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x AX449572 (1-2752)

QY 1 GlnLysIleSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
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Db 2494 CAGAAGATAATTTCCAGCTGTGACCCACCTGTAGCGGGTGGCGACTGCGGACTCTG 2553

QY 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
|||||
Db 2554 GCCCAGAAATCCACCTGACAGCATCTCAGCTTTTGTGCTCCCAAGCCAGCCGCCACA 2613

QY 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
|||||
Db 2614 GCCATGATCCTCAACCTGTGGAGGCGGGCACTTCCCAAGCGCAACTCAGCCAGCTG 2673

QY 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
|||||
Db 2674 GCTGACAGAGTGGCTGGACTGGCCAGCAGACGCTGGCTTTTACAGTGTGCGAGGCT 2733

QY 81 Glu 81
|||||
Db 2734 GAG 2736

RESULT 4
LOCUS CQ730306 2784 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 16240 from Patent WO02068579.
ACCESSION CQ730306
VERSION CQ730306.1 GI:42303801

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 16240 06-SEP-2002;
PE Corporation (NY) (US)

FEATURES
source
1..2784
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.44e-41 Length: 2784
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x CQ730306 (1-2784)

QY 1 GlnLysIleSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
|||||
Db 2536 CAGAAGATAATTTCCAGCTGTGACCCACCTGTAGCGGGTGGCGACTGCGGACTCTG 2595

QY 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
|||||
Db 2596 GCCCAGAAATCCACCTGACAGCATCTCAGCTTTTGTGCTCCCAAGCCAGCCGCCACA 2655

QY 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
|||||
Db 2656 GCCATGATCCTCAACCTGTGGAGGCGGGCACTTCCCAAGCGCAACTCAGCCAGCTG 2715

QY 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
|||||
Db 2716 GCTGACAGAGTGGCTGGACTGGCCAGCAGACGCTGGCTTTTACAGTGTGCGAGGCT 2775

QY 81 Glu 81
|||||
Db 2776 GAG 2778

RESULT 5
LOCUS AX527916 2881 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 1 from Patent WO0229038.
ACCESSION AX527916
VERSION AX527916.1 GI:25172359

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Herrmann, J.L., Rastelli, L. and Shimkets, R.A.

TITLE Novel proteins and nucleic acids encoding same and antibodies directed against these proteins
JOURNAL Patent: WO 0229038-A 1 11-APR-2002; Curagen Corporation (US)
FEATURES
source 1..2881
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1.5e-41 Length: 2881
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x AX527916 (1-2881)
Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2538 CAGAAGATAATTTCCAGCTGGACCCACCTGTAGCGGGTGGCGACTGCGGACTCTG 2597
Qy 21 AlaGlnlyLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2598 GCCCAGAAACTCCACCTGGACGAGCATCTCAGCTTCTTTGGCTCCAGCCCGCCACCA 2657
Qy 41 AlaMetlleLeuAsnLeuTrpGluAlaAArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2658 GCCATGATCTCTCAACCTGTGGAGCGGGGACTTCCCCACGCGCAACCTCAGCGAGCTG 2717
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2718 GCTGCAGCAGTGGCTGGAGTGGCGCAGCCAGACGCTGGCTCTTCACAGTGTGCGAGGCT 2777
Qy 81 Glu 81
Db 2778 GAG 2780
RESULT 6
AX367094
LOCUS AX367094 3580 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 13 from Patent WO0198354.
ACCESSION AX367094
VERSION AX367094.1 GI:18855296
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Griffin,J.A., Kallick,D.A., Tribouley,C.M., Yue,H., Nguyen,D.B., Tang,Y.T., Lal,P., Policky,J.L., Azimzai,Y., Lu,D.A., Graul,R., Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O., Patterson,C., Yang,J., Xu,Y., Warren,B.A., Ding,L. and Sanjanwalla,M.S.
TITLE Receptors
JOURNAL Patent: WO 0198354-A 13 27-DEC-2001; Incyte Genomics, Inc. (US)
FEATURES
source 1..3580
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 6052371CB1"
ORIGIN
Alignment Scores:
Pred. No.: 1.92e-41 Length: 3580
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x AX367094 (1-3580)
Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2284 CAGAAGATAATTTCCAGCTGGACCCACCTGTAGCGGGTGGCGACTGCGGACTCTG 2343
Qy 21 AlaGlnlyLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2344 GCCCAGAAACTCCACCTGGACGAGCATCTCAGCTTCTTTGGCTCCAGCCCGCCACCA 2403
Qy 41 AlaMetlleLeuAsnLeuTrpGluAlaAArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2404 GCCATGATCTCTCAACCTGTGGAGCGGGGACTTCCCCACGCGCAACCTCAGCGAGCTG 2463
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2464 GCTGCAGCAGTGGCTGGACTGGCGCAGCAGCTGGCTCTTCACAGTGTGCGAGGCT 2523
Qy 81 Glu 81
Db 2524 GAG 2526
RESULT 7
AX054976
LOCUS AX054976 9700 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 91 from Patent WO0073328.
ACCESSION AX054976
VERSION AX054976.1 GI:12228344
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Crielinge,W., Roelens,I., Bogaert,T. and Verwaerde,P.
TITLE Unc-5 constructs and screening methods
JOURNAL Patent: WO 0073328-A 91 07-DEC-2000; Devgen NV (BE)
FEATURES
source 1..9700
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="plasmid pGC1037"
ORIGIN
Alignment Scores:
Pred. No.: 6.03e-41 Length: 9700
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x AX054976 (1-9700)
Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 1064 CAGAAGATAATTTCCAGCTGGACCCACCTGTAGCGGGTGGCGACTGCGGACTCTG 1123
Qy 21 AlaGlnlyLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1124 GCCCAGAAACTCCACCTGGACGAGCATCTCAGCTTCTTTGGCTCCAGCCCGCCACCA 1183
Qy 41 AlaMetlleLeuAsnLeuTrpGluAlaAArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 1184 GCCATGATCTCTCAACCTGTGGAGCGGGGACTTCCCCACGCGCAACCTCAGCGAGCTG 1243
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80

Db 1244 GCTGCAGCAGTGGCTGGACTGGCGCCAGACGTCGTCCTTTCACAGTGTGCGAGGCT 1303
Qy 81 Glu 81
Db 1304 GAG 1306

RESULT 8
AX268596
LOCUS AX268596
DEFINITION Sequence 15 from Patent WO0175440.
ACCESSION AX268596
VERSION AX268596.1 GI:16541710
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1
AUTHORS Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and Pratt,J.Y.
TITLE Schizophrenia related genes
JOURNAL Patent: WO 0175440-A 15 11-OCT-2001;
WELFIDE CORPORATION (JP)
FEATURES
source
1..2697
/organism="Rattus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10118"

ORIGIN
Alignment Scores:
Pred. No.: 5.46e-40 Length: 2697
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservative: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x AX268596 (1-2697)
Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrrpArgThrleu 20
Db 2449 CAAAAGATCATGCGCAGCTCGGACCCACCTTCGCGGGCGCGACTGGAGAACTCTA 2508
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
Db 2509 GCCCAGAAACTTCACCTCGACAGCCATCTTAGCTTCTTTGCTCCAGCCCGCCCTACA 2568
Qy 41 AlaMetlleLeuAsnLeuTrrpGluAlaAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2569 GCCATGATCTCAACCTTATGGGAGGCACGGCAGCTTCCCAAGCGCAACTCGGCCAGCTG 2628
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2629 GCAGCAGCTGTGGCGGAGCTGGCCCAACAGATGCTGCGCTTTCACGGTGTGCGAGGCC 2688

Qy 81 Glu 81
Db 2689 GAG 2691

RESULT 9
RNU87305
LOCUS RNU87305
DEFINITION Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds.
ACCESSION U87305
VERSION U87305.1 GI:2055391
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 2697)
AUTHORS Leonardo,B.D., Hinck,L., Masu,M., Keino-Masu,K., Ackerman,S.I. and Tessier-Lavigne,M.
TITLE Vertebrate homologues of C. elegans UNC-5 are candidate netrin receptors
JOURNAL Nature 386 (6627), 833-838 (1997)
MEDLINE 97271897
PUBMED 9126742

REFERENCE 2 (bases 1 to 2697)
AUTHORS Leonardo,B.D., Hinck,L., Masu,M., Keino-Masu,K. and Tessier-Lavigne,M.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus, San Francisco, CA 94143-0452, USA
FEATURES
Location/Qualifiers
source
1..2697
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/tissue_type="brain and ventral spinal cord"
/dev_stage="18 day embryo and 13 day embryo"

CDS
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/codon_start=1
/product="transmembrane receptor UNC5H1"
/protein_id="AAB57678.1"
/db_xref="GI:2055392"
/translation="MAVRPGLPVLILGIVLAWLGRSGAQQSATVANPVGANPDLLP
HFLVPEBDVYIVKNKPVLLVCKAVPATQIFPKCNQWVRQVDHVIERTSDSSGLPTM
EVRINVSQVQEVKVGLEEVWCQVAMSSGCTTKSQAYIRIAYLRKNPEOEPLAKEV
SLEQIVLPCRPPEGIPPAEVEWLRNEDLVDPDNPVYITREHSLVVRQARLATAN
YTCVAKNIVARRRSTAAVIVYNGSWSTWTSVCSASCGRGWOKRSRSTNPAPLN
GGAFCEQNVQKTACATLCPVDGSSWSKWSACGLDCTHWRSECDSPAPRNGEEC
RGADLLRNTCTDLCHTASCPEDVALYIGLVAVAVCLFLLLALLGLTYCRKKEGLD
DVADSSILTSGFQPVSIKSKADNPILLTIQDLSLTSTTTTQYGLSCSDQDGPSPFOL
SNCHLSPLAGSRHTLHSSPTSEADPVSLSTONVPSRPRCTSNMAYGTFFLGG
RLMIPNTGISLLIPDPAIPRNGIYEIYTLHKPEDVRLPLACQTLTSFVSCGPGPV
LLTRPVILAMDHCQSPSPDSWSLRKKQSCGSEGWEDVHLHSESHLYYQLEAGAC
YVFTQELGRFALVGEALSVAATLRLLLPAPVACTSLEYINRVYCLDHTDHALKEVV
QLEKQLAGQLIQEPRVLFKDSYHNLRSLSDHVPSSLSKSLYSQIPIPFVHWGT
QOYLHCTFTLERNASTDLACKVMQVEGDGOSFNINFTIKDTFAELLALSEEG
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AMILNLNWARHPFNGNLGQLAAAVAGLQPDAGLFTVSEAC"

ORIGIN
Alignment Scores:
Pred. No.: 5.46e-40 Length: 2697
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservative: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x RNU87305 (1-2697)
Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrrpArgThrleu 20
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Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
Db 2509 GCCCAGAAACTTCACCTCGACAGCCATCTTAGCTTCTTTGCTCCAGCCCGCCCTACA 2568
Qy 41 AlaMetlleLeuAsnLeuTrrpGluAlaAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2569 GCCATGATCTCAACCTTATGGGAGGCACGGCAGCTTCCCAAGCGCAACTCGGCCAGCTG 2628
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2629 GCAGCAGCTGTGGCGGAGCTGGCCCAACAGATGCTGCGCTTTCACGGTGTGCGAGGCC 2688

Qy 81 Glu 81
Db 2689 GAG 2691


```

RESULT 10
BD057524
LOCUS      BD057524
DEFINITION Netrin receptors.
ACCESSION  BD057524
VERSION    BD057524.1 GI:22603130
KEYWORDS   JP 2001505062-A/1.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 3014)
AUTHORS    Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.
TITLE      Netrin receptors
JOURNAL    Patent: JP 2001505062-A 1 17-APR-2001;
            THE REGENTS OF THE UNIV OF CALIFORNIA
COMMENT    PN JP 2001505062-A/1
            PD 17-APR-2001
            PF 19-FEB-1998 JP 1998536840
            PR 19-FEB-1997 US 08/808982
            PI MARC TESSIER LAVIGNE,DAVID E LEONARDO,LINDSAY HINCK,MASAYUKI
            PI MASU.
            PC C07K1/00,C07K14/00,C07H21/02,C07H21/04,G01N33/53 CC
            Strandedness: Double;
            CC Topology: Linear;
            FH Key Location/Qualifiers.
FEATURES             Location/Qualifiers
     source           1..3014
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.:          6.2e-40          Length:          3014
Score:              410.00           Matches:          78
Percent Similarity: 97.53%           Conservative:     1
Best Local Similarity: 96.30%         Mismatches:      2
Query Match:        96.93%           Indels:          0
DB:                  6               Gaps:            0

US-10-624-932C-2_COPY_817_897 (1-81) x BD057524 (1-3014)
Qy      1 GlnlylIleSerSerLeuAspProCysArgArgGlyAlaAepTtpArgThrIeu 20
        |||||
Db      2449 CAAAGAATCATCGGACGCTCGACCCACCTCCGACGGCGCGCGGCTGGAGAACTCTA 2508
        |||||
Qy      21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
        |||||
Db      2509 GCCCAGAAACTTCACCTGGACAGGCATCTTAGCTTCTTGGCTCCAGCCCGCCCTACA 2568
        |||||
Qy      41 AlaMetIleLeuAsnLeuTtpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
        |||||
Db      2569 GCCATGATCTCTCAACCTATGGGAGGCGACGGCACTTCCCAACGGCAACCTCGGCAGCTG 2628
        |||||
Qy      61 AlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
        |||||
Db      2629 GCACGAGCTGTGGCGGAGCTGGCGGCAACCAAGATGCTGGCCTCTTTCACGGTGTGGAGGCC 2688
        |||||
Qy      81 Glu 81
        |||
Db      2689 GAG 2691

RESULT 11
BC058084
LOCUS      BC058084
DEFINITION Mus musculus unc-5 homolog A (C. elegans), mRNA (cDNA clone
ACCESSION  MGC:66671 IMAGE:6813463), complete cds.
VERSION    BC058084.1 GI:34784158
KEYWORDS   MGC.
SOURCE     Mus musculus (house mouse)

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ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3844)

REFERENCE
AUTHORS

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.I., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smaluis,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 3844)
Strausberg,R.
Direct Submission
Submitted (08-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lilisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smaluis, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 126 Row: b Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23346570.

FEATURES
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gene

CDS


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Db 2800 GCCATGATCTCTCAACCTATGGAGCGCGGCACTTCCCAACGCGCAACCTCGGCAGCTG 2859
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RESULT 13
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LOCUS Mus musculus mRNA for mKIAA1976 protein.
DEFINITION AK122575
ACCESSION AK122575
VERSION AK122575.1 GI:28972881
KEYWORDS FLI CDNA.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Okazaki,N., Kikuno,R., Ohara,R., Inamoto,S., Aizawa,H., Yuasa,S., Nakajima,D., Nagase,T., Ohara,O. and Koga,H.
TITLE Prediction of the coding sequences of mouse homologues of KIAA gene: II. The complete nucleotide sequences of 400 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries
JOURNAL DNA Res. 10, 35-48 (2003)
REFERENCE 2 (bases 1 to 4294)
AUTHORS Okazaki,N., Kikuno,R., Nagase,T., Ohara,O. and Koga,H.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2003) Hisashi Koga, Kazusa DNA Research Institute, Laboratory for Genome Informatics; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
COMMENT (E-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918) The CREATE program supported by Japan science and technology corporation; cDNA full insert sequencing: Kazusa DNA Research Institute; cDNA library construction, clone selection and 5'- & 3'-end one pass sequencing.
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Query Match: 96.93% Indels: 0
DB: 10 Gaps: 0

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Qy 21 AlaGlnlyLeuHisLeuAenSerHisLeuSerPhePheAlaSerIysProSerProThr 40
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Db 3121 GCCATGATCTCTCAACCTATGGAGCGCGGCACTTCCCAACGCGCAACCTCGGCAGCTG 3180
Qy 61 AlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 3181 GCCCAGCTGTGGCGGAGTGGCGAGCCAGATGCTGGCTCTTCCACCGTGTACAGAGGCC 3240
Qy 81 Glu 81
Db 3241 GAG 3243

RESULT 14
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LOCUS Netrin receptors.
DEFINITION BD057525
ACCESSION BD057525
VERSION BD057525.1 GI:22603131
KEYWORDS JP 2001505062-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1787)
AUTHORS Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.
TITLE Netrin receptors
JOURNAL Patent: JP 2001505062-A 2 17-APR-2001;
THE REGENTS OF THE UNIV OF CALIFORNIA
COMMENT PN JP 2001505062-A/2
PD 17-APR-2001
PF 19-FEB-1998 JP 1998536840
PR 19-FEB-1997 US 08/808982
PI MARC TESSIER LAVIGNE, DAVID E LEONARDO, LINDSAY HINCK, MASAYUKI
PI MASU
PI KAZUKO KEINO MASU
PC C07K1/00, C07K14/00, C07K17/00, C07H21/02, C07H21/04, G01N33/53 CC
CC Topology: Linear;
FH Key Location/Qualifiers.
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 Db 1660 CTGAG 1664
 RESULT 15
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 AC135142
 ACCESSION AC135142.2
 VERSION GI:25007239
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 171419)
 Muzny, D. Marie, Metzker, M. Lee, Abramzon, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
 Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
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 Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
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 Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
 Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
 Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
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 Yu, F., Zhang, J., Zhou, J., Zhou, S., Zhao, S., Dunn, D., von
 Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
 Weinstock, G. and Gibbs, R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 171419)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (08-OCT-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 171419)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Nov 15, 2002 this sequence version replaced gi:23578050.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: KCMS
 Center clone name: CH230-169PS
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 127081 bases at least Q40
 Consensus quality: 131254 bases at least Q30
 Consensus quality: 133849 bases at least Q20
 Estimated insert size: 128800; sum-of-contigs estimation
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 consists of 9 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.
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 * 18755 18854: gap of unknown length
 * 18855 147860: contig of 129006 bp in length
 * 147861 147960: gap of unknown length
 * 147961 159835: contig of 11875 bp in length
 * 159836 159935: gap of unknown length
 * 159936 161085: contig of 1150 bp in length
 * 161086 161185: gap of unknown length
 * 161186 162489: contig of 1304 bp in length
 * 162490 162589: gap of unknown length

* 162590 164048: contig of 1459 bp in length
* 164049 164148: gap of unknown length
* 164149 165318: contig of 1170 bp in length
* 165319 165418: gap of unknown length
* 165419 167567: contig of 2149 bp in length
* 167568 167668: gap of unknown length
* 167669 171419: contig of 3752 bp in length.

FEATURES

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ORIGIN

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Query Match:	84.93%	Indels:	48
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US-10-624-932C-2_COPY_817_897 (1-81) x AC135142 (1-171419)

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Search completed: September 9, 2005, 09:42:59
Job time : 3399.92 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 8, 2005, 20:54:46 ; Search time 418.907 Seconds
(without alignments)
1144.643 Million cell updates/sec

Title: US-10-624-932C-2_COPY_817_897

Perfect score: 423
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Scoring table: BLOSUM62
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	423	100.0	2697	6 ABK52891	Abk52891 Human net
5	423	100.0	2752	6 ABK37922	Abk37922 cDNA enco

6	423	100.0	2752	12 ADH71617	Adh71617 Human gen
7	423	100.0	2880	12 ADH71633	Adh71633 Human gen
8	423	100.0	2881	6 ABK49422	Abk49422 DNA enco
9	423	100.0	2881	10 ADG42568	Adg42568 Novel hum
10	423	100.0	2881	12 ADH71635	Adh71635 Human gen
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18	423	100.0	2881	12 ADH71639	Adh71639 Human gen
19	423	100.0	2881	12 ADH71643	Adh71643 Human gen
20	423	100.0	2881	12 ADH71625	Adh71625 Human gen
21	423	100.0	2881	12 ADH71647	Adh71647 Human gen
22	423	100.0	2907	4 AAK52261	Aak52261 Human pol
23	423	100.0	3561	12 ADL06497	Adl06497 Human tum
24	423	100.0	3580	6 ABK15169	Abk15169 Human R&P
25	423	100.0	9700	4 AAC90958	Aac90958 Plaemid p
26	410	96.9	2697	2 AAS16843	Aas16843 Rat netri
27	410	96.9	3014	2 AAV52940	Av52940 Rat UNC-5
28	409	96.7	2881	12 ADH71649	Adh71649 Human gen
29	393	92.9	1269	4 AAS34792	Aas34792 cDNA enco
30	393	92.9	1269	10 ADC45950	Adc45950 Human neo
31	376	88.9	1787	2 AAV52941	Aav52941 Human UNC
32	368	87.0	1321	4 AAH99530	Aah99530 Human pro
33	364	86.1	574	4 AAD16536	Aad16536 Human nov
34	364	86.1	574	4 AAS34948	Aas34948 cDNA enco
35	364	86.1	574	6 ABS64126	Ab64126 Human apo
36	364	86.1	574	10 ADC46106	Adc46106 Human neo
37	364	86.1	574	10 AAD60435	Aad60435 Human sec
C 38	357.5	84.5	6522	8 AAL51204	Aal51204 Human gen
C 39	357.5	84.5	9582	4 AAD16560	Aad16560 Human nov
C 40	357.5	84.5	9582	6 ABS64150	Ab64150 Human apo
C 41	357.5	84.5	9582	10 AAD60459	Aad60459 Human sec
C 42	351.5	83.1	18772	4 AAD16561	Aad16561 Human nov
C 43	351.5	83.1	18772	6 ABS64151	Ab64151 Human apo
C 44	351.5	83.1	18772	10 AAD60460	Aad60460 Human sec
C 45	305	72.1	276	6 ABK52895	Abk52895 Human net

ALIGNMENTS

RESULT 1
ADH71623
ID ADH71623 standard; DNA; 2463 BP.
XX
AC ADH71623;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21h SEQ ID NO:519.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386376P.

PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-038796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387669P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388036P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389146P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 18-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 15-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
PR (CURA-) CURAGEN CORP.

XX PI Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CM, Voss EZ, Zhong M;
PI Zhong H;
XX WPI: 2004-081935/08.
DR P-PSDB; ADH71624.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX Example 21; SEQ ID NO 519; 1880pp; English.
PS
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2463 BP; 470 A; 828 C; 721 G; 444 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.03e-43 Length: 2463
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x ADH71623 (1-2463)
Qy 1 GlnLysIleIleSerLeuAspProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2212 CAGAAGATAATTTCCAGCTGGACCCACCTGTAGGGGGTGGCGACTGGCGACTCTG 2271
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2272 GCCCAGAAACTCCACCTGGACGCCATCTCAGCTTCCTTGCTCCAGCCAGCCCCACA 2331
Qy 41 AlaMetIleLeuAenLeuTrpGluAlaArgHisPheProAenGlyAenLeuSerGlnLeu 60
Db 2332 GCCATGATCTCTCAACCTGTGGAGCGCGGCACATTCCTCCACACGCAACTCAGGAGCTG 2391
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2392 GCTGACGAGTGGCTGGACTGGGCACGACAGCTGGCTTCTTTCACAGTGTGGAGGCT 2451
Qy 81 Glu 81
Db 2452 GAG 2454
RESULT 2
ADH71621
ID ADH71621 standard; DNA; 2575 BP.
XX
AC ADH71621;

QY 1 GlnLysIleIleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20


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|||||
2256 CAGAGATAATTTCCAGGCTGGACCCACCTGTAGCGGGGTGCGACTGCGGACTCTG 2315
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2316 GCCCAGAAATCCACCTGACAGGACATCTCAGCTCTTTTGGCTCCAGGCCAGCCACCA 2375
Qy 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2376 GCCATGATPCTCAACCTGTGGAGGCGCGGACATTCCTCCCAACGGCAACCTCAGCCAGCTG 2435
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2436 CTGCGAGCAGTGGCTGGAGCTGGCGCAGCCAGCGCTGGCCCTCTTCACAGTGTGAGGCT 2495
Qy 81 Glu 81
Db 2496 GAG 2498
RESULT 3
ADN95100
ID ADN95100 standard; DNA; 2635 BP.
XX AC ADN95100;
XX DT 01-JUL-2004 (first entry)
XX DE Human LEC gene sequence SeqID22.
XX KW growth; differentiation; blood endothelial cell; BEC;
XX KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
XX KW lymphatic growth agent; VEGF-C; VEGF-D; angiogenic; cytotatic;
XX KW vasotrophic; antiinflammatory; gene therapy; endothelial cell disorder;
XX KW inflammatory disease; cancer metastasis; lymphatic system; gene; de;
XX KW human.
XX OS Homo sapiens.
XX FN WO2003080640-A1.
XX PD 02-OCT-2003.
XX PF 07-MAR-2003; 2003WO-US006900.
XX PR 07-MAR-2002; 2002US-0363019P.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (LICN) LICENTIA LTD.
XX PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
XX WPI; 2003-876899/81.
XX DR P-PSDB; ADN95115.
XX PS Claim 23; SEQ ID NO 22; 176pp; English.
```

This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that the LEC protein is not VEGFR-3; and administering to the subject a composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of compounds with an angiogenic, cytotatic, vasotrophic or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphoedema, in screening for an endothelial cell disorder or predisposition to the disorder or in monitoring the efficacy or toxicity

of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the differential modulation of blood vessel endothelial cell or lymphatic vessel endothelial cell growth or differentiation. The lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as various inflammatory diseases and cancer metastasis via the lymphatic system. The present sequence is that of a human LEC/BEC differentially expressed gene which is related to the method of the invention. Note: The expressed data for this patent did not form part of the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 2635 BP; 483 A; 935 C; 722 G; 495 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.13e-43	Length:	2635
Score:	423.00	Matches:	81
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-10-624-932C-2_COPY_817_897 (1-81) x ADN95100 (1-2635)

Qy	1	GlnLysIleLeuSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu	20
Db	1379	CAGAAAGATAATTTCCAGCTGGACCCACCTGTAGCGGGGTGCGACTGCGGACTCTG	1438
Qy	21	AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr	40
Db	1439	GCCCAGAAATCCACCTGGACGCATCTCAGCTCTTTTGGCTCCAGGCCAGCCACCA	1498
Qy	41	AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu	60
Db	1499	GCCATGATCTCAACCTGTGGAGCGCGGACCTTCCCAACGGCAACCTCAGCCAGCTG	1558
Qy	61	AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla	80
Db	1559	GCTGCGAGTGGCTGGACTGGCGCAGCCAGACCTGGCCCTCTTCACAGTGTGAGGCT	1618
Qy	81	Glu 81	
Db	1619	GAG 1621	

RESULT 4

ABK52891
ID ABK52891 standard; DNA; 2697 BP.

XX AC ABK52891;

XX DT 27-AUG-2002 (first entry)

XX DE Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.

XX KW Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human; neurotropic; neuroprotective; cytotatic; antiparkinsonian; cerebroprotective; cancer; central nervous system; CNS; stroke; Parkinson's disease; multiple sclerosis; Alzheimer's disease.

XX OS Homo sapiens.

PH	Key	Location/Qualifiers
FT	CDS	1..2697
FT		/*tag= a
FT		/product= "Netrin binding membrane receptor UNC5H-1"

XX PN WO200233080-A2.

XX PD 25-APR-2002.

XX PF 15-OCT-2001; 2001WO-EP011891.

XX

PR 16-OCT-2000; 2000US-0240061P.
XX (FARB) BAYER AG.
XX Koehler RH;
XX WPI; 2002-463314/49.
DR P-PSDB; AAU97899.
XX Novel human netrin binding membrane receptor polypeptide and
PT polynucleotides for identifying modulating agents useful in treating
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
PT Alzheimer's disease.
XX Claim 1; Fig 1; 94pp; English.
XX This invention relates to the DNA and protein sequences of a novel
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC sequence of the invention is useful as a probe for detecting a nucleic
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
CC of the invention are useful to screen for agents which decrease the
CC activity of the UNC5H-1 protein. The sequences are also useful for
CC screening agents which regulate (modulate) the activity of the protein of
CC the invention. A pharmaceutical composition containing the protein of the
CC invention or a reagent that modulates the activity of the UNC5H-1 protein
CC may be useful for treating a UNC5H-1 dysfunction related disease such as
CC cancer or a central nervous system (CNS) disorders (e.g. Parkinson's
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
CC proteins comprising the UNC5H-1 protein are useful for generating
CC antibodies and for in various assay systems, and the protein can be used
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
CC of the invention is useful for detecting a coding sequence for the UNC5H-
CC 1 protein. The present sequence represents a DNA sequence encoding the
CC human netrin binding membrane receptor UNC5H-1 protein of the invention
XX
SQ Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.16e-43 Length: 2697
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x ABK52891 (1-2697)

QY 1 GlnLysIleLeuSerSerLeuAspProProCysArgArgGlyAlaAspTrrpArgThrIeu 20
DB 2449 CAGAAAGATTAATTCAGCCTGGACCACCCCTGTAGCGGGGGTGGCGGACTGGCGGACTCTG 2508

QY 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
DB 2509 GCCCAGAAATCCACCTGACAGCCATCTCAGCTTCTTTGGCTCCAGCCAGCCGCCA 2568

QY 41 AlaMetIleLeuAsnLeuTrrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
DB 2569 GCCATGATCCTCAACTGTGGGAGCGCGGCACTTCCCAACGGCAACTCAGCCAGCTG 2628

QY 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
DB 2629 GCTGCAGCAGTGCTGGAGTGGCCAGCCAGCAGCTGGCCCTTTCACAGTGTCCGAGGCT 2688

QY 81 Glu 81
DB 2689 GAG 2691

RESULT 5
ID ABK37922
XX ABK37922 standard; CDNA; 2752 BP.
XX
AC ABK37922;
XX

DT 21-MAY-2002 (first entry)
XX CDNA encoding Human protein NOV1.
XX Human; NOVX; as; gene; cardiomyopathy; atherosclerosis; diabetes;
KW cell signal processing disorder; metabolic disorder; obesity; infection;
KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
KW psychosis; neurological disorder; anxiety; schizophrenia;
KW manic depression; dementia; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome; gene therapy.
XX
XX Homo sapiens.
XX WO200210216-A2.
XX
XX 07-FEB-2002.
XX
XX 30-JUL-2001; 2001WO-US024225.
XX
XX 28-JUL-2000; 2000US-0221409P.
PR 04-AUG-2000; 2000US-0222840P.
PR 04-AUG-2000; 2000US-0223752P.
PR 04-AUG-2000; 2000US-0223762P.
PR 04-AUG-2000; 2000US-0223769P.
PR 04-AUG-2000; 2000US-0223770P.
PR 14-AUG-2000; 2000US-0225148P.
PR 15-AUG-2000; 2000US-0225392P.
PR 15-AUG-2000; 2000US-0225470P.
PR 16-AUG-2000; 2000US-0225697P.
PR 01-FEB-2001; 2001US-0263662P.
PR 05-APR-2001; 2001US-0281645P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Padigar M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;
PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;
XX
XX WPI; 2002-180074/23.
DR P-PSDB; AAU85403.
XX
XX New isolated cytoplasmic, nuclear, membrane bound, or secreted
PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
PT immune disorders.
XX
XX Claim 9; Page 9-10; 213pp; English.
XX
XX The invention relates to an isolated cytoplasmic, nuclear, membrane
CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
CC form. Also included are the nucleic acids encoding the NOVX proteins, a
CC vector comprising the nucleic acid, a cell comprising the vector, an anti-
CC NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
CC antibody are useful for treating or preventing a NOVX-associated
CC disorder, where the disorder is selected from cardiomyopathy,
CC atherosclerosis, diabetes, a disorder related to cell signal processing
CC and metabolic pathway modulation, metabolic disorders, obesity,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,
CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases, bacterial, fungal, protozoal and viral infections, pain,
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
CC disease, multiple sclerosis, Albrit Hereditary Osteodystrophy, angina
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC hypertrophy, and psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC nucleic acid is useful in gene therapy. The present sequence encodes a

```
CC NOVX protein
XX SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,2e-43 Length: 2752
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x ABK37922 (1-2752)

Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrrArgThrIeu 20
Db 2494 CAGAAGATAAATTCACGCTGACCCACCTGTAGCGGGGTGCCGACTCGGACACTGTG 2553
Qy 21 AlaGlnLysLeuHleLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2554 GCCCAGAAACCTCCACCTGGACGACCATCTCAGCTTCCTTGCTCCAAAGCCAGCCCA 2613
Qy 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2614 GCCATGATCCTCAACCTGTGGAGGGCGGCACCTTCCCAACGGCAACCTTCAGCCAGCTG 2673
Qy 61 AlalaAlaValAlaGlyIeuGlyGlnProaspAlaGlyLeuPheThrValSerGluAla 80
Db 2674 GCTGCAGCAGTGCTGGAGCTGGCGCAGCCAGACGCTGGCCCTTCACAGTGTGCGAGGCT 2733
Qy 81 Glu 81
Db 2734 GAG 2736

RESULT 6
ADH71617
ID ADH71617 standard; DNA; 2752 BP.
XX ADH71617;
AC ADH71617;
XX
XX 25-MAR-2004 (first entry)
XX
XX Human gene of the invention NOV21e SEQ ID NO:513.
XX
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
XX anorectic; antidiabetic; antimicrobial; antipneumic; gene therapy;
XX vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
XX obesity; diabetes; infectious disease; metabolic syndrome X;
XX dyslipidaemia.
XX
XX Homo sapiens.
XX
XX WO2003102155-A2.
XX
XX 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
XX
XX 03-JUN-2002; 2002US-0385120P.
XX 04-JUN-2002; 2002US-0385784P.
XX 05-JUN-2002; 2002US-0386041P.
XX 06-JUN-2002; 2002US-0386047P.
XX 07-JUN-2002; 2002US-0386376P.
XX 08-JUN-2002; 2002US-0386453P.
XX 09-JUN-2002; 2002US-0386864P.
XX 10-JUN-2002; 2002US-0387016P.
XX 11-JUN-2002; 2002US-0387796P.
XX 12-JUN-2002; 2002US-0388161P.
XX 13-JUN-2002; 2002US-0388616P.
XX 14-JUN-2002; 2002US-0389120P.
XX 15-JUN-2002; 2002US-0389144P.
XX 16-JUN-2002; 2002US-0389146P.
XX 17-JUN-2002; 2002US-0389729P.
XX 18-JUN-2002; 2002US-0389742P.
XX 19-JUN-2002; 2002US-0389884P.
XX 20-JUN-2002; 2002US-0390066P.
XX 21-JUN-2002; 2002US-0390209P.
XX 22-JUN-2002; 2002US-0390763P.
XX 23-JUN-2002; 2002US-0396706P.
XX 24-JUN-2002; 2002US-0401628P.
XX 25-JUN-2002; 2002US-0402156P.
XX 26-JUN-2002; 2002US-0402256P.
XX 27-JUN-2002; 2002US-0402389P.
XX 28-JUN-2002; 2002US-0402786P.
XX 29-JUN-2002; 2002US-0402816P.
XX 30-JUN-2002; 2002US-0402821P.
XX 31-JUN-2002; 2002US-0402832P.
XX 32-JUN-2002; 2002US-0403458P.
XX 33-JUN-2002; 2002US-0403459P.
XX 34-JUN-2002; 2002US-0403531P.
XX 35-JUN-2002; 2002US-0403532P.
XX 36-JUN-2002; 2002US-0403563P.
XX 37-JUN-2002; 2002US-0403617P.
XX 38-JUN-2002; 2002US-0403617P.
XX 39-JUN-2002; 2002US-0406182P.
XX 40-JUN-2002; 2002US-0406355P.
XX 41-JUN-2002; 2002US-0406240P.
XX 42-JUN-2002; 2002US-0406240P.
XX 43-JUN-2002; 2002US-0410084P.
XX 44-JUN-2002; 2002US-0412528P.
XX 45-JUN-2002; 2002US-0412731P.
XX 46-JUN-2002; 2002US-0414801P.
XX 47-JUN-2002; 2002US-0414839P.
XX 48-JUN-2002; 2002US-0414840P.
XX 49-JUN-2002; 2002US-0414954P.
XX 50-JUN-2002; 2002US-0417186P.
XX 51-JUN-2002; 2002US-0417406P.
XX 52-JUN-2002; 2002US-0420639P.
XX 53-JUN-2002; 2002US-0421156P.
XX 54-JUN-2002; 2002US-0422690P.
XX 55-JUN-2002; 2002US-0423130P.
XX 56-JUN-2002; 2002US-0423798.
XX 57-JUN-2002; 2002US-0423798P.
XX 58-JUN-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
XX Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
XX Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
XX Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
XX MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
XX Padigar M, Patturajan M, Pena CEA, Peyman JA, Raha D, Raetelli L;
XX Rieger DK, Rothenberg ME, Scioe P, Shenoy SG, Shinkets RA;
XX Smithson G, Spytek KA, Stone DU, Vernet CAM, Voss EZ, Zhong M;
XX Zhong H;
```

XX WP1; 2004-081935/08.
DR P-PSDB; ADH71618.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 513; 1880pp; English.
PS
PS The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaeamic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.2e-43 Length: 2752
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932c-2_COPY_817_897 (1-81) x ADH71617 (1-2752)

QY 1 GlnLysIleLeuSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
DB 2494 CAGAGAGATATTTCCAGCTGAGCCACCTGTAGCGGGTGCCGACTGGCGGACTCTG 2553
QY 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerIysProSerProThr 40
DB 2554 GCCCAGAAATCCACCTGACAGCCATCTCAGCTTCTTGGCTCCCAAGCCAGCCCA 2613
QY 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
DB 2614 GCCATGATCCTCAACCTGTGGAGGCGCGGCACCTTCCCCAACGGCAACCTCAGCAGCTG 2673
QY 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
DB 2674 GCTGACGACGTGGCTGGACTGGCCAGCAGACGCTGGGCTCTTACAGTGTTCGGAGGCT 2733
QY 81 Glu 81
DB 2734 GAG 2736

RESULT 7
ADH71633
ID ADH71633 standard; DNA; 2880 BP.
XX
XX ADH71633;
XX
XX 25-MAR-2004 (first entry)
XX
XX Human gene of the invention NOV21m SEQ ID NO:529.
XX
XX da; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX OS Homo sapiens.
XX PN WO2003102155-A2.
XX PD 11-DEC-2003.
XX
XX 03-JUN-2003; 2003WO-US017430.
XX
XX 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386798P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390008P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402258P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.

PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.
XX
XX
PI Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Carterton E, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VV, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CE, Feyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
XX
DR WPI; 2004-081935/08.
DR P-PSDB; ADH71634.
XX
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 529; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2880 BP; 527 A; 984 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.27e-43 Length: 2880
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x ADH71633 (1-2880)

QY 1 GlnlysllelleSerSerleuAspProProCysArgArgGlyAlaAspTrrpArgThrIeu 20
Db 2537 CAGAGATAAATTTCCAGCTGTCAGACCCACCTGTAGCGGGGTGCGACTGCGGACTCTG 2596

QY 21 AlaGlnlyslleuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
Db 2597 GCCCAGAAATCCACTCGACAGCCATCTCAGCTCTTTGGCTCCAGCCGCCGCCACA 2656

QY 41 AlaMetIleLeuAsnLeuTrrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2657 GCCATGATCCTCAACCTGTGGGAGCGGGCACTTCCGCAACGGCAACCTCAGCCAGCTG 2716

QY 61 AlaAlaAlaValAlaAlaGlyLeuGlyGlnProAspAlaGlyIeuPheThrValSerGluAla 80
Db 2717 GCTTCAGCAGTGGCTGGACTGGGGCAGCCAGCCTGGCCTCTTCACAGTGTGGAGGCT 2776

QY 81 Glu 81
Db 2777 GAG 2779

RESULT 8
ABK49422
ID ABK49422 standard; DNA; 2881 BP.
XX
AC ABK49422;
XX
DT 15-JUL-2002 (first entry)
XX
DE DNA encoding human UNC5-like protein NOV1.
XX
KW Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;
KW cell signal processing; metabolic pathway modulation; cancerous tissue;
KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;
KW chromosome 13; gene; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 87..2786
FT /*tag= a
FT /product= "Human UNC5-like protein NOV1"
XX
PN WO200229038-A2.
XX
PD 11-APR-2002.
XX
XX 04-OCT-2001; 2001WO-US031377.
XX
PR 04-OCT-2000; 2000US-0237862P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Herrmann JL, Rastelli L, Shimkets RA;
XX
XX WPI; 2002-340104/37.
DR P-PSDB; AAU79939.
XX
PT Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for
PT treating cardiomyopathy, atherosclerosis, and cancer.
XX
PS Claim 8; Page 7-8; 180pp; English.
XX
CC The present invention relates to a new NOVX polypeptide having a 900
CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)
CC residue amino acid sequence, as given in the specification. The novel
CC polypeptide, and its encoding polynucleotide, are used to treat
CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell
CC signal processing and metabolic pathway modulation, in a human. Detecting
CC the polypeptide or polynucleotide is useful for identifying cancerous
CC tissue. The antibody can be used to treat diabetes or cancer. The host
CC cells can be used to produce non-human transgenic animals useful in drug
CC screening. The present nucleic acid sequence is that of the human UNC5-
CC like NOV1 gene located on chromosome 13. This sequence encodes the human
CC UNC5-like protein NOV1 of the invention
XX
SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.27e-43 Length: 2881
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x ABK49422 (1-2881)

QY	1	GlnLysIleIleSerSerLeuAspProProCysArgArgGlyAlaAspTIPArgThrLeu	20
Db	2538	CAGAGATATTTCCAGCTTGGACCCACCTGTAGGCGGGTGCCTGACTGGCGACTCTG	2597
QY	21	AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr	40
Db	2598	GCCCAGAAACTCCACCTGGACAGCATCTCAGCTTCTTTGCTTCAAAGCCAGCCCCACA	2657
QY	41	AlaMetIleLeuAsnLeuTTPGluAlaArgHisPheProHengLysAsnLeuSerGlnLeu	60
Db	2658	GCCATGATCTCAACCTGTGGAGGCCGCGACATTCCCCAAACGCAACCTCAGCCAGCTG	2717
QY	61	AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla	80
Db	2718	GCTGCAGCACTGGCTGGACTGGGCCAGCCAGACGCTGGCTCTTTCACAGTGTGGAGGCT	2777
QY	81	Glu 81	
Db	2778	GAG 2780	
RESULT 9			
ADG42568			
ID	ADG42568	standard; cDNA; 2881 BP.	
XX	AC	ADG42568;	
XX	DT	26-FEB-2004 (first entry)	
XX	XX	Novel human NOV1 cDNA.	
XX	XX	cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;	
KW	KW	NOVX-associated disorder; cancer; human; gene; ss.	
XX	XX	Homo sapiens.	
OS	OS	US2003204052-A1.	
PN	PN	30-OCT-2003.	
PD	PD	04-OCT-2001; 2001US-00970944.	
XX	XX	04-OCT-2000; 2000US-0237862P.	
XX	XX	(HERR/) HERRMANN J L.	
PA	PA	(RAST/) RASTELLI L.	
PA	PA	(SHIM/) SHIMKETS R A.	
XX	XX	Herrmann JL, Rastelli L, Shimkets RA;	
PI	PI	WPI; 2003-900673/82.	
DR	DR	P-PSDB; ADG42569.	
XX	XX	New NOVX gene or NOVX-specific antibody, useful for preparing a	
PT	PT	composition for treating or preventing a NOVX-associated disorder, e.g.,	
PT	PT	cancer.	
XX	XX	Claim 9; SEQ ID NO 1; 118pp; English.	
PS	PS	The invention describes a new isolated polypeptide comprising: a	
XX	XX	polypeptide or its mature form comprising a sequence not given in the	
CC	CC	specification; or a variant of (A), where one or more amino acid residues	
CC	CC	in the variant differs in no more than 15% from the amino acid sequence	
CC	CC	of the mature form. The pharmaceutical composition may be administered	
CC	CC	via oral, transdermal, rectal or parenteral route. The polypeptide,	
CC	CC	nucleic acid or antibody is useful for preparing a composition for	
CC	CC	treating or preventing a NOVX-associated disorder, e.g., cancer. This	
CC	CC	sequence encodes a human NOVX protein.	
XX	XX	Sequence 2881 BP; 526 A; 987 C; 866 G; 502 T; 0 U; 0 Other;	
SQ	SQ		

PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
FA (CURA-) CURAGEN CORP.
XX
XX
PI Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Hermann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI MacLachlan T, Malyankar UM, Mexick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CE, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
XX Zhong H;
XX
DR WPI; 2004-081935/08.
DR P-PSDB; ADH71636.
XX

PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 531; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipidemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing.
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.27e-43 Length: 2881
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x ADH71635 (1-2881)

Qy 1 GlnLysIleLeuSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2538 CAGAGATAATTTCCAGCTGGACCCACCTGTAGGGGGGTGCGGACTGTG 2597

Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2598 GCCCAGAAACTCCACCTGGACGCACTCAGCTTCTTGGCTCCAGCCGAGCCCA 2657

Qy 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2658 GCCATGATCTCAACCTGTGGAGGGCGGCACCTTCCCAAGCGCAACCTCAGCCAGCTG 2717

Qy 61 AlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2718 GCTGCAGCAGTGGCTGGACTGGGCGCAGCAGCTGGCCTCTTTTACAGTGTGAGGCT 2777

Qy 81 Glu 81
Db 2778 GAG 2780

RESULT 11
ADH71637
ID ADH71637 standard; DNA; 2881 BP.
XX
AC ADH71637;
XX
DT 25-MAR-2004 (first entry)
XX
DB Human gene of the invention NOV21o SEQ ID NO:533.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipidemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.

XX	11-DEC-2003.		
PD			
XX	03-JUN-2003; 2003WO-US017430.		
PF			
XX	03-JUN-2002; 2002US-0385120P.		
XX	04-JUN-2002; 2002US-0385784P.		
PR	05-JUN-2002; 2002US-0386041P.		
PR	05-JUN-2002; 2002US-0386047P.		
PR	06-JUN-2002; 2002US-0386376P.		
PR	06-JUN-2002; 2002US-0386453P.		
PR	06-JUN-2002; 2002US-0386864P.		
PR	06-JUN-2002; 2002US-0387016P.		
PR	07-JUN-2002; 2002US-0386796P.		
PR	07-JUN-2002; 2002US-0386816P.		
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PR	07-JUN-2002; 2002US-0386942P.		
PR	07-JUN-2002; 2002US-0386971P.		
PR	07-JUN-2002; 2002US-0387262P.		
PR	08-JUN-2002; 2002US-0296960P.		
PR	10-JUN-2002; 2002US-0387400P.		
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PR	11-JUN-2002; 2002US-0387696P.		
PR	11-JUN-2002; 2002US-0387702P.		
PR	11-JUN-2002; 2002US-0387836P.		
PR	11-JUN-2002; 2002US-0387859P.		
PR	12-JUN-2002; 2002US-0387933P.		
PR	12-JUN-2002; 2002US-0387934P.		
PR	12-JUN-2002; 2002US-0387960P.		
PR	12-JUN-2002; 2002US-0388022P.		
PR	12-JUN-2002; 2002US-0388096P.		
PR	13-JUN-2002; 2002US-0389123P.		
PR	14-JUN-2002; 2002US-0389118P.		
PR	14-JUN-2002; 2002US-0389120P.		
PR	14-JUN-2002; 2002US-0389144P.		
PR	14-JUN-2002; 2002US-0389146P.		
PR	17-JUN-2002; 2002US-0389723P.		
PR	17-JUN-2002; 2002US-0389742P.		
PR	18-JUN-2002; 2002US-0389884P.		
PR	19-JUN-2002; 2002US-0390006P.		
PR	19-JUN-2002; 2002US-0390209P.		
PR	21-JUN-2002; 2002US-0390763P.		
PR	17-JUL-2002; 2002US-0396708P.		
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PR	09-AUG-2002; 2002US-0402156P.		
PR	09-AUG-2002; 2002US-0402256P.		
PR	09-AUG-2002; 2002US-0402389P.		
PR	12-AUG-2002; 2002US-0402786P.		
PR	12-AUG-2002; 2002US-0402816P.		
PR	12-AUG-2002; 2002US-0402821P.		
PR	12-AUG-2002; 2002US-0402832P.		
PR	13-AUG-2002; 2002US-0403448P.		
PR	13-AUG-2002; 2002US-0403459P.		
PR	13-AUG-2002; 2002US-0403531P.		
PR	13-AUG-2002; 2002US-0403532P.		
PR	13-AUG-2002; 2002US-0403563P.		
PR	13-AUG-2002; 2002US-0406317P.		
PR	15-AUG-2002; 2002US-0406117P.		
PR	26-AUG-2002; 2002US-0406182P.		
PR	26-AUG-2002; 2002US-0406355P.		
PR	27-AUG-2002; 2002US-0406240P.		
PR	12-SEP-2002; 2002US-0410084P.		
PR	20-SEP-2002; 2002US-0412528P.		
PR	23-SEP-2002; 2002US-0412731P.		
PR	30-SEP-2002; 2002US-0414801P.		
PR	30-SEP-2002; 2002US-0414839P.		
PR	30-SEP-2002; 2002US-0414840P.		
PR	30-SEP-2002; 2002US-0414954P.		
PR	09-OCT-2002; 2002US-0417186P.		
PR	09-OCT-2002; 2002US-0417406P.		
PR	23-OCT-2002; 2002US-0420639P.		
PR	28-OCT-2002; 2002US-0421156P.		
PR	31-OCT-2002; 2002US-0422690P.		
PR	01-NOV-2002; 2002US-04231130P.		
PR	05-NOV-2002; 2002US-04232798.		
PR	05-NOV-2002; 2002US-0423798P.		
PR	12-NOV-2002; 2002US-0425453P.		
XX	(CURA-) CURAGEN CORP.		
XX			
PI	Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;		
PI	Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;		
PI	Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;		
PI	Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;		
PI	MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;		
PI	Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raba D, Rastelli L;		
PI	Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;		
PI	Smithson G, Spytek KA, Stone DU, Vernet CAM, Voss EZ, Zhong M;		
PI	Zhong H;		
XX			
XX	WPI; 2004-081935/08.		
DR	P-PSDB, ADH71638.		
XX			
XX	New NOVX polypeptides and nucleic acid molecules useful for preventing or		
PT	treating NOVX-associated disorders, e.g. cancer, diabetes, infection or		
PT	obesity, and in chromosome mapping, tissue typing or pharmacogenomics.		
XX			
PS	Example 21; SEQ ID NO 533; 1880pp; English.		
XX			
CC	The invention relates to a novel isolated polypeptide (NOVX). A		
CC	polypeptide of the invention has cytostatic, immunomodulator,		
CC	neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and		
CC	antilipaeamic activity, and may have a use in gene therapy, and as a		
CC	vaccine. The polypeptides are encoded by NOVX polynucleotides comprising		
CC	any of the 303 fully defined nucleotide sequences given in the		
CC	specification. The polypeptide is useful in the manufacture of a		
CC	medicament for treating a syndrome associated with a human disease. The		
CC	polypeptide, polynucleotide and antibody are useful in diagnosing,		
CC	treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,		
CC	Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious		
CC	diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are		
CC	further used as hybridisation probes, in chromosome mapping, tissue		
CC	typing, preventive medicine, and pharmacogenomics. The present sequence		
CC	encodes a NOVX polypeptide of the invention.		
XX			
SQ	Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;		
	Alignment Scores:		
	Pred. NO.:	1.27e-43	Length: 2881
	Score:	423.00	Matches: 81
	Percent Similarity:	100.00%	Conservative: 0
	Best Local Similarity:	100.00%	Mismatches: 0
	Query Match:	100.00%	Indels: 0
	DB:	12	Gaps: 0
	US-10-624-932C-2_COPY_817_897 (1-81) x ADH71637 (1-2881)		
Qy	1 GlnlyseilleSerSerLeuAspProCysArgGlyAlaAspTrpArgThrLeu 20		
Db	2338 CAGAAGATAATTTCCAGCTGGAGCCACCTGTAGGCGGGTGGCGACTGTG 2597		
Qy	21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40		
Db	2598 GCCCAGAAACTCCACCTGGACGACCATCTCAGCTTCTTTCCTCCAGCCGCCACCA 2657		
Qy	41 AlaMetIleLeuAenLeuTrpGluAlaArgHisPheProAenGlyAenLeuSerGlnLeu 60		
Db	2658 GCCATGATCTCTCACTGTGGAGCGCGGACCTTCCCAACGCGCAACTCAGCAGCTG 2717		
Qy	61 AlaalaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80		
Db	2718 GCTGACGAGTGTGGACTGGCGGCAGCCAGACGCTGGCTCTTTTCACAGTGTGGAGGCT 2777		

Qy 81 Glu 81
Db 2778 GAG 2780
RESULT 12
ID ADH71641 standard; DNA; 2881 BP.
XX AC ADH71641;
XX DT 25-MAR-2004 (first entry)
XX DE Human gene of the invention NOV21q SEQ ID NO:537.
XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
XX WO2003102155-A2.
XX PD 11-DEC-2003.
XX PF 03-JUN-2003; 2003WO-US017430.
XX PR 03-JUN-2002; 2002US-0385120P.
XX PR 04-JUN-2002; 2002US-0385784P.
XX PR 05-JUN-2002; 2002US-0386041P.
XX PR 05-JUN-2002; 2002US-0386047P.
XX PR 06-JUN-2002; 2002US-0386376P.
XX PR 06-JUN-2002; 2002US-0386453P.
XX PR 06-JUN-2002; 2002US-0386864P.
XX PR 07-JUN-2002; 2002US-0387016P.
XX PR 07-JUN-2002; 2002US-0386881P.
XX PR 07-JUN-2002; 2002US-0386931P.
XX PR 07-JUN-2002; 2002US-0386942P.
XX PR 07-JUN-2002; 2002US-0386971P.
XX PR 07-JUN-2002; 2002US-0387262P.
XX PR 08-JUN-2002; 2002US-0387600P.
XX PR 10-JUN-2002; 2002US-0387400P.
XX PR 10-JUN-2002; 2002US-0387535P.
XX PR 11-JUN-2002; 2002US-0387610P.
XX PR 11-JUN-2002; 2002US-0387625P.
XX PR 11-JUN-2002; 2002US-0387634P.
XX PR 11-JUN-2002; 2002US-0387668P.
XX PR 11-JUN-2002; 2002US-0387698P.
XX PR 11-JUN-2002; 2002US-0387702P.
XX PR 11-JUN-2002; 2002US-0387836P.
XX PR 11-JUN-2002; 2002US-0387859P.
XX PR 12-JUN-2002; 2002US-0387933P.
XX PR 12-JUN-2002; 2002US-0387934P.
XX PR 12-JUN-2002; 2002US-0388022P.
XX PR 12-JUN-2002; 2002US-0388096P.
XX PR 13-JUN-2002; 2002US-03891123P.
XX PR 14-JUN-2002; 2002US-0389118P.
XX PR 14-JUN-2002; 2002US-0389120P.
XX PR 14-JUN-2002; 2002US-0389144P.
XX PR 14-JUN-2002; 2002US-0389146P.
XX PR 17-JUN-2002; 2002US-0389729P.
XX PR 17-JUN-2002; 2002US-0389742P.
XX PR 18-JUN-2002; 2002US-0389884P.
XX PR 19-JUN-2002; 2002US-0390006P.
XX PR 19-JUN-2002; 2002US-0390209P.
XX PR 21-JUN-2002; 2002US-0390763P.
XX PR 17-JUL-2002; 2002US-0396706P.
XX PR 06-AUG-2002; 2002US-0401628P.
XX PR 09-AUG-2002; 2002US-0402156P.

PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 15-AUG-2002; 2002US-0406317P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX PA (CURA-) CURAGEN CORP.

XX PI Alsbrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ,
Catterton E, Chapeval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
Gusev VI, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
Zhong H;
XX XX

XX WPI; 2004-081935/08.
DR P-PSDB; ADH71642.

XX PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX PS Example 21; SEQ ID NO 537; 1880pp; English.

XX CC The invention relates to a novel isolated polypeptide (NOVX). A
polypeptide of the invention has cytostatic, immunomodulator,
neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
antilipemic activity, and may have a use in gene therapy, and as a
vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
any of the 303 fully defined nucleotide sequences given in the
specification. The polypeptide is useful in the manufacture of a
medicament for treating a syndrome associated with a human disease. The
polypeptide, polynucleotide and antibody are useful in diagnosing.
treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
further used as hybridisation probes, in chromosome mapping, tissue
typing, preventive medicine, and pharmacogenomics. The present sequence
encodes a NOVX polypeptide of the invention.

XX SQ Sequence 2881 BP; 526 A; 986 C; 867 G; 502 T; 0 U; 0 Other;

Alignment Scores:


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Pred. No.: 1.27e-43 Length: 2881
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932c-2_COPY_817_897 (1-81) x ADH71641 (1-2881)

QY 1 GlnLysIleLeuSerLeuAspProProCysArgArgGlyAlaAspTriArgThrLeu 20
DB 2538 CAGAGATAATTTCCAGCTGACCCACCTCTAGCGGGTCCGACTGGCGGACTCTG 2597
QY 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerIleProSerProThr 40
DB 2598 GCCCAGAAACTCACCTGCACAGCCATCTCAGCTTCTTGCCCTCCAAAGCCAGCCCCACA 2657
QY 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
DB 2658 GCCATGATCCTCAACCTGTGGAGCGCGGCACCTTCCCAAGCGCAACTCAGCCAGCTG 2717
QY 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
DB 2718 GCTGAGCAGTGGCTGGACTGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCCGAGGCT 2777
QY 81 Glu 81
DB 2778 GAG 2780

RESULT 13
ADH71609
ID ADH71609 standard; DNA; 2881 BP.
XX
XX AC ADH71609;
XX
XX DT 25-MAR-2004 (first entry)
XX
XX DE Human gene of the invention NOV21a SEQ ID NO:505.
XX
XX KW ds; Gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO2003102155-A2.
XX
XX PD 11-DEC-2003.
XX
XX PF 03-JUN-2003; 2003WO-US017430.
XX
XX PR 03-JUN-2002; 2002US-0385120P.
XX PR 04-JUN-2002; 2002US-0385784P.
XX PR 05-JUN-2002; 2002US-0386041P.
XX PR 06-JUN-2002; 2002US-0386047P.
XX PR 06-JUN-2002; 2002US-0386453P.
XX PR 06-JUN-2002; 2002US-0386864P.
XX PR 06-JUN-2002; 2002US-0387016P.
XX PR 07-JUN-2002; 2002US-0386796P.
XX PR 07-JUN-2002; 2002US-0386816P.
XX PR 07-JUN-2002; 2002US-0386931P.
XX PR 07-JUN-2002; 2002US-0386943P.
XX PR 07-JUN-2002; 2002US-0386971P.
XX PR 07-JUN-2002; 2002US-0387262P.
XX PR 08-JUN-2002; 2002US-0296960P.
XX PR 10-JUN-2002; 2002US-0387400P.
XX PR 10-JUN-2002; 2002US-0387535P.
XX PR 11-JUN-2002; 2002US-0387610P.
XX PR 11-JUN-2002; 2002US-0387625P.
XX PR 11-JUN-2002; 2002US-0387634P.
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PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
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PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
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PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-0423798.
PR 12-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
XX Caterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
XX Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
XX Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
XX MacLachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
XX Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Raetelli L;
XX Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shinkets RA;
XX Smithson G, Spytek KA, Stone DU, Vernet CAM, Voss EZ, Zhong M;
XX Zhong H;
XX
XX WPI; 2004-081935/08.
XX P-PSDB; ADH71610.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
```

PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX Example 21; SEQ ID NO 505; 1880pp; English.

XX The invention relates to a novel isolated polypeptide (NOVX). A
XX polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaeamic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing.
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.27e-43 Length: 2881
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservations: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x ADH71609 (1-2881)

Qy 1 GlnYslllelSerSerLeuAspProCysArgArgGlyAlaAspTrpArgThrIeu 20
Db 2538 CAGAAGATAATTCCAGCTGGACCCACCTGTAGCGGGTGGCGACTGCGGACTGTG 2597
Qy 21 AlaGlnYsLeuHsLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2598 GCCAGAAACTCCACCTGGAGCAGCACTTCAGTCTTTGGCTCCAGCCGAGCCCA 2657
Qy 41 AlaMetlleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2658 GCCATGATCTCAACCTGTGGAGGGCGGCACCTCCCAACGGCAACCTCAGCCAGCTG 2717
Qy 61 AlalalaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2718 GCTGAGCAGTGGCTGGACTGGCGCAGCCAGACGCTGGCCCTTTTACAGTGTGCGAGGCT 2777
Qy 81 Glu 81
Db 2778 GAG 2780

RESULT 14

ADH71629

ID ADH71629 standard; DNA; 2881 BP.

XX ADH71629;

XX 25-MAR-2004 (first entry)

XX Human gene of the invention NOV21k SEQ ID NO:525.

XX ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaeamic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX Homo sapiens.

XX WO2003102155-A2.

PN

XX

PD 11-DEC-2003.
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PI Ettenberg S, Gangoli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
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PI Smithson G, Spytek KA, Stone DJ, Vernhet CAM, Voss EZ, Zhong M;
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XX WPI; 2004-081935/08.
DR P-PSDB; ADH71630.
XX
XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX Example 21; SEQ ID NO 525; 1880pp; English.
XX
XX The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator, and
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
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XX Sequence 2881 BP; 526 A; 986 C; 868 G; 501 T; 0 U; 0 Other;
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KW anorectic; antidiabetic; antimicrobial; antilipemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
XX OS Homo sapiens.
XX
XX PN WO2003102155-A2.
XX
XX PD 11-DEC-2003.
XX
XX PF 03-JUN-2003; 2003WO-US017430.
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XX PR 03-JUN-2002; 2002US-0385120P.
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PR 09-AUG-2002; 2002US-0402156P.
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GenCore version 5.1.6
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Listing first 45 summaries

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ALIGNMENTS

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; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: Leonardo, E. David
; APPLICANT: Hink, Lindsay
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:

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; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; Patent No. 627585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-306-902A-1
Alignment Scores:
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Score: 410.00 Matches: 78
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Best Local Similarity: 96.30% Mismatches: 2
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; Sequence 2, Application US/08808982
; Patent No. 5939271
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; APPLICANT: Hink, Lindsey
; APPLICANT: Masu, Masayuki
; APPLICANT: Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,982
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
;
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TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
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SEQUENCE CHARACTERISTICS:
LENGTH: 1787 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
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DB: 0
Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-08-808-982-2 (1-1787)

Qy 1 GlnlysllelleSerSerLeuAspProProCybArgArgGlyAlaAspTTPArgThrLeu 20
Db 1420 CAGAGATAATTTCCAGCTGGACCCACCCTGTAGCGGGTGGCGACTGGCGACTCTG 1479
Qy 21 AlaGlnlyLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1480 GCCCAGAACTCCACCTGGACGCCATCTCAGCTTCTTTGGCTTCCAGCCGCCACCA 1539
Qy 41 AlaMetlleLeuAenLeuTTPGluAlaArgHisPheProAenGlyAenLeuSerGlnLeu 60
Db 1540 GCCATGATCTCCACCTGTGGAGCGCGGCACCTTCCCAACGGCACTCAGCCAGCTG 1599
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeu-PheThrVal-SerGluA 80
Db 1600 GCTGCAGCAGTGGCTGGGACTGGCCAGCAGACGGTGGCTTCTTTCACAGTGTTCGGAGG 1659
Qy 80 laGlu 81
Db 1660 CTGAG 1664

RESULT 4

US-09-306-902A-2
Sequence 2, Application US/09306902A
Patent No. 6277585

GENERAL INFORMATION:

APPLICANT: Tessier-Lavigne, Marc

Leonardo, E. David

Hink, Lindsey

Masu, Masayuki

Kazuko, Keino-Masu

Neurin Receptors

TITLE OF INVENTION: 9

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/306,902A

FILING DATE: 07-May-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UC96-217

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1787 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-306-902A-2

Alignment Scores:
Pred. No.: 4.06e-42 Length: 1787
Score: 376.00 Matches: 77
Percent Similarity: 92.77% Conservative: 0
Best Local Similarity: 92.77% Mismatches: 4
Query Match: 88.89% Indels: 2
DB: 0
Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-306-902A-2 (1-1787)

Qy 1 GlnlysllelleSerSerLeuAspProProCybArgArgGlyAlaAspTTPArgThrLeu 20
Db 1420 CAGAGATAATTTCCAGCTGGACCCACCCTGTAGCGGGTGGCGACTGGCGACTCTG 1479
Qy 21 AlaGlnlyLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1480 GCCCAGAACTCCACCTGGACGCCATCTCAGCTTCTTTGGCTTCCAGCCGCCACCA 1539
Qy 41 AlaMetlleLeuAenLeuTTPGluAlaArgHisPheProAenGlyAenLeuSerGlnLeu 60
Db 1540 GCCATGATCTCCACCTGTGGAGCGCGGCACCTTCCCAACGGCACTCAGCCAGCTG 1599
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeu-PheThrVal-SerGluA 80
Db 1600 GCTGCAGCAGTGGCTGGGACTGGCCAGCAGACGGTGGCTTCTTTCACAGTGTTCGGAGG 1659
Qy 80 laGlu 81
Db 1660 CTGAG 1664

RESULT 5

US-09-949-016-16776/c

Sequence 16776, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 16776

LENGTH: 19326

TYPE: DNA

ORGANISM: Human

US-09-949-016-16776

Alignment Scores:

Pred. No.: 4.42e-38 Length: 19326

Score: 357.50 Matches: 81

Percent Similarity: 50.94% Conservative: 0

Best Local Similarity: 50.94% Mismatches: 0

Query Match:	84.52%	Indels:	78
DB:	4	Gaps:	1
US-10-624-932C-2_COPY_817_897 (1-81) x US-09-949-016-16776 (1-19326)			
Qy	1	GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu	20
Db	18788	CAGAAGATAAATTTTCAGCCTGGACCCACCTGTATGGCGGGGTGCCGACTGGCGGACTCTG	18729
Qy	21	AlaGlnlyslLeuHisLeuAsp-	27
Db	18728	GCCAGAAACTTCCACCTGGACAGGTGGCGGGAGAGGGGCAGAGAGGCCCTTGGCGAGGCC	18669
Qy	27	-----	27
Db	18668	ACCACAGTCCTGCCCGCGGGGTGGTGAGGTGGACAGGAGGCCCTGTGGGGCGCTG	18609
Qy	27	-----	27
Db	18608	TGCCGCATCTACTAGTGGCGGGCAGTCATTGTGTTTGGCTTCGGGAGGCCCTGCCCC	18549
Qy	27	-----	27
Db	18548	GGGTGGGCCAGAGGGGGGCACGAGGTGTACGTGGGGCCAGGCCAGGCTGTGACGGGCC	18489
Qy	28	-----SerHisLeuSerPheAlaSerLySProSerProThrAlaMetIl	43
Db	18488	CCCTCCCTCCACAGCCATCTCAGCTCTTTTGGCTTCCAAAGCCAGCCCAACGATCAT	18429
Qy	43	eLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeuAlaAlaAl	63
Db	18428	CCTCAACCTGTGGAGGGCGGCACCTTCCCAACGGCAACCTCAGCCAGCTGGCTGCAGC	18369
Qy	63	avalalacglyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGlu	81
Db	18368	AGTGGCTGGACTGGGCCAGCAGACGCTGGGCTCTTACAGTGTGAGGCTGAG	18314
RESULT 6			
US-09-949-016-4794			
; Sequence 4794, Application US/09949016			
; Patent No. 6812339			
; GENERAL INFORMATION:			
; APPLICANT: VENTER, J. Craig et al.			
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED			
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF			
; FILE REFERENCE: CL001307			
; CURRENT APPLICATION NUMBER: US/09/949,016			
; CURRENT FILING DATE: 2000-04-14			
; PRIOR APPLICATION NUMBER: 60/241,755			
; PRIOR FILING DATE: 2000-10-20			
; PRIOR APPLICATION NUMBER: 60/237,768			
; PRIOR FILING DATE: 2000-10-03			
; PRIOR APPLICATION NUMBER: 60/231,498			
; PRIOR FILING DATE: 2000-09-08			
; NUMBER OF SEQ ID NOS: 207012			
; SOFTWARE: FASTSEQ for Windows Version 4.0			
; SEQ ID NO 4794			
; LENGTH: 3008			
; TYPE: DNA			
; ORGANISM: Human			
US-09-949-016-4794			
Alignment Scores:			
Pred. No.:			
Score:			
Percent Similarity:			
Best Local Similarity:			
Query Match:			
DB:			
Length:			
Matches:			
Conservative:			
Mismatches:			
Indels:			
Gaps:			
US-10-624-932C-2_COPY_817_897 (1-81) x US-09-949-016-4794 (1-3008)			
Qy	1	GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu	20

Qy 1 GlnYsIleLeSerSerLeuAspProProCysArgArgGlyAlaAspTArgThrLeu 20
Db 2583 CAGAGAGCTGCAACAGCGCTGACGCCCAACTCAGCGGGCAATGACTGGCGGTGTG 2642
Qy 21 AlaGlnYsLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2643 GCACAGAGCTCTCCATGACCGGTACCTGAACCTACCTGCGCCCAAGCTAGTCCACA 2702
Qy 41 AlaMetIleLeuAsnLeuTIPgluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2703 GCGGTGATCTAGACCTCTGGGAAGCTCGGCAGCAGGATGATGGGGACCTCAACAGCCTG 2762
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProlep 71
Db 2763 GCCAGTGCCTTGGAGAGATGGCAAGAGTGAG 2795

RESULT 8
US-09-306-902A-3
; Sequence 3, Application US/09306902A
; Patent No. 6277585
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/306,902A
; FILING DATE: 07-May-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-306-902A-3

Alignment Scores:
Pred. No.: 3,95e-17 Length: 2831
Score: 198.00 Matches: 38
Percent Similarity: 76.08% Conservative: 16
Best Local Similarity: 53.52% Mismatches: 17
Query Match: 46.81% Indels: 0
DB: 3 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-306-902A-3 (1-2831)

Qy 1 GlnYsIleLeSerSerLeuAspProProCysArgArgGlyAlaAspTArgThrLeu 20
Db 2583 CAGAGAGCTGCAACAGCGCTGACGCCCAACTCAGCGGGCAATGACTGGCGGTGTG 2642

Db 2583 CAGAGAGCTGCAACAGCGCTGACGCCCAACTCAGCGGGCAATGACTGGCGGTGTG 2642
Qy 21 AlaGlnYsLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2643 GCACAGAGCTCTCCATGACCGGTACCTGAACCTACCTGCGCCCAAGCTAGTCCACA 2702
Qy 41 AlaMetIleLeuAsnLeuTIPgluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2703 GCGGTGATCTAGACCTCTGGGAAGCTCGGCAGCAGGATGATGGGGACCTCAACAGCCTG 2762
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProlep 71
Db 2763 GCCAGTGCCTTGGAGAGATGGCAAGAGTGAG 2795

RESULT 9
US-09-969-532-31
; Sequence 31, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encod
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-31

Alignment Scores:
Pred. No.: 3,04e-16 Length: 1968
Score: 190.00 Matches: 36
Percent Similarity: 70.37% Conservative: 21
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 44.92% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-31 (1-1968)

Qy 1 GlnYsIleLeSerSerLeuAspProProCysArgArgGlyAlaAspTArgThrLeu 20
Db 1681 CAGCGATTTGCTGCTACATTTGATACCCCAATGCAAGGCAAGGATGCGAGATGTTA 1740
Qy 21 AlaGlnYsLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1741 GCACAGAAAAACAGCATCAACAGGAATTTATCTTTTCGCTACACAAAGTAGCCCATCT 1800
Qy 41 AlaMetIleLeuAsnLeuTIPgluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 1801 GCTGTGATTTGAACCTGTGGAGAGCTGTCATCAGCATGATGGTGATCTTGACCTCCCTG 1860
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProaspAlaGlyLeuPheThrValSerGluAla 80
Db 1861 GCTGTGCTTGAAGAGATTTGGGAGGACACACAGAAACTCTCAACATTTTCAGATTC 1920

Alignment Scores:
Pred. No.: 81 Glu 81
Score: 1921 CAG 1923
Percent Similarity: 76.08% Conservative: 16
Best Local Similarity: 53.52% Mismatches: 17
Query Match: 46.81% Indels: 0
DB: 3 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-31 (1-1968)
; Sequence 29, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encod

```
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-29

Alignment Scores:
Pred. No.: 3,13e-16 Length: 2001
Score: 190.00 Matches: 36
Percent Similarity: 70.37% Conservativity: 21
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 44.92% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-29 (1-2001)

Qy 1 GlnlystlelleSerSerLeuAspProProCysArgArgGlyAlaAspTtpArgThrLeu 20
Db 1714 CAGCGGATTGTGCTACATTGATACCCCAATGCCAAGGCAAGGACTGGCAGATGTTA 1773

Qy 21 AlaGlnlystlelleSerSerLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1774 GCACAGAAAACAGCATCAACAGGAATTATCTATTTCGCTACACAAAGTAGCCCATCT 1833

Qy 41 AlaMetlleLeuAenLeuTtpGluAlaArgHisPheProAenglyAenLeuSerGlnLeu 60
Db 1834 GCTGTCATTTGAACCTGTGGGAGCTCGTCATCAGCATGATGTTGATCTTGCCTCGT 1893

Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 1994 GCCTGTGCCCTTGAAGAGATTGGGAGGACACACACAGAAACTCTCAAAACATTTCAAGATCC 1953

Qy 81 Glu 81
Db 1954 CAG 1956

RESULT 11
US-09-969-532-27
; Sequence 27, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-27

Alignment Scores:
Pred. No.: 3,13e-16 Length: 2010
Score: 190.00 Matches: 36
Percent Similarity: 70.37% Conservativity: 21
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 44.92% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-27 (1-2010)
```

```
Qy 1 GlnlystlelleSerSerLeuAspProProCysArgArgGlyAlaAspTtpArgThrLeu 20
Db 1723 CAGCGGATTGTGCTACATTGATACCCCAATGCCAAGGCAAGGACTGGCAGATGTTA 1782

Qy 21 AlaGlnlystlelleSerSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1783 GCACAGAAAACAGCATCAACAGGAATTATCTATTTCGCTACACAAAGTAGCCCATCT 1842

Qy 41 AlaMetlleLeuAenLeuTtpGluAlaArgHisPheProAenglyAenLeuSerGlnLeu 60
Db 1843 GCTGTCATTTGAACCTGTGGGAGCTCGTCATCAGCATGATGTTGATCTTGCCTCGT 1902

Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 1903 GCCTGTGCCCTTGAAGAGATTGGGAGGACACACACAGAAACTCTCAAAACATTTCAAGATCC 1962

Qy 81 Glu 81
Db 1963 CAG 1965

RESULT 12
US-09-969-532-25
; Sequence 25, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6777232el Human Membrane Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 2043
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-25

Alignment Scores:
Pred. No.: 3,2e-16 Length: 2043
Score: 190.00 Matches: 36
Percent Similarity: 70.37% Conservativity: 21
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 44.92% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-25 (1-2043)

Qy 1 GlnlystlelleSerSerLeuAspProProCysArgArgGlyAlaAspTtpArgThrLeu 20
Db 1756 CAGCGGATTGTGCTACATTGATACCCCAATGCCAAGGCAAGGACTGGCAGATGTTA 1815

Qy 21 AlaGlnlystlelleSerSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 1816 GCACAGAAAACAGCATCAACAGGAATTATCTATTTCGCTACACAAAGTAGCCCATCT 1875

Qy 41 AlaMetlleLeuAenLeuTtpGluAlaArgHisPheProAenglyAenLeuSerGlnLeu 60
Db 1876 GCTGTCATTTGAACCTGTGGGAGCTCGTCATCAGCATGATGTTGATCTTGCCTCGT 1935

Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 1936 GCCTGTGCCCTTGAAGAGATTGGGAGGACACACACAGAAACTCTCAAAACATTTCAAGATCC 1995

Qy 81 Glu 81
Db 1996 CAG 1998

RESULT 13
```

```
US-09-969-532-15
; Sequence 15, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: NO. 6777232el Human Membrane Proteins and Polynucleotides Encod
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2661
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-15

Alignment Scores:
Pred. No.: 4.66e-16 Length: 2661
Score: 190.00 Matches: 36
Percent Similarity: 70.37% Conservativeness: 21
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 44.92% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-15 (1-2661)
Qy 1 GlnlylIleSerSerLeuAspProProCysArgArgGlyAlaAspTTPArgThrLeu 20
Db 2374 CAGCGGATTTGCTGCTACATTTGATACCCCAATGCCAAAGGCAAGGACTGGCAGATGTTA 2433
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2434 GCACAGAAAAACAGCATCAACAGGAATTTATCTTATTCGCTACACAAGTAGCCCATCT 2493
Qy 41 AlaMetIleLeuAsnLeuTTPGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2494 GCTGTCATTTGAACCTTGGAGAGATTGGGAGGACATCATCAGCATGATGGTGATCTTGGACTCCCTG 2553
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2554 GCCTGTGCCCTTGAAGAGATTGGGAGGACACACACAGAAACTCTCAAAACATTTCAAGATCC 2613
Qy 81 Glu 81
Db 2614 CAG 2616

RESULT 14
US-09-969-532-13
; Sequence 13, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: NO. 6777232el Human Membrane Proteins and Polynucleotides Encod
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2694
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-13

Alignment Scores:
Pred. No.: 4.74e-16 Length: 2694
```

```
Score: 190.00 Matches: 36
Percent Similarity: 70.37% Conservativeness: 21
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 44.92% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-13 (1-2694)
Qy 1 GlnlylIleSerSerLeuAspProProCysArgArgGlyAlaAspTTPArgThrLeu 20
Db 2407 CAGCGGATTTGCTGCTACATTTGATACCCCAATGCCAAAGGCAAGGACTGGCAGATGTTA 2466
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2467 GCACAGAAAAACAGCATCAACAGGAATTTATCTTATTCGCTACACAAGTAGCCCATCT 2526
Qy 41 AlaMetIleLeuAsnLeuTTPGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2527 GCTGTCATTTGAACCTTGGAGAGATTGGGAGGACATCATCAGCATGATGGTGATCTTGGACTCCCTG 2586
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2587 GCCTGTGCCCTTGAAGAGATTGGGAGGACACACACAGAAACTCTCAAAACATTTCAAGATCC 2646
Qy 81 Glu 81
Db 2647 CAG 2649

RESULT 15
US-09-969-532-11
; Sequence 11, Application US/09969532
; Patent No. 6777232
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; TITLE OF INVENTION: NO. 6777232el Human Membrane Proteins and Polynucleotides Encod
; FILE REFERENCE: LEX-0244-USA
; CURRENT APPLICATION NUMBER: US/09/969,532
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 60/237,280
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2703
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-969-532-11

Alignment Scores:
Pred. No.: 4.77e-16 Length: 2703
Score: 190.00 Matches: 36
Percent Similarity: 70.37% Conservativeness: 21
Best Local Similarity: 44.44% Mismatches: 24
Query Match: 44.92% Indels: 0
DB: 4 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-969-532-11 (1-2703)
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Db 2416 CAGCGGATTTGCTGCTACATTTGATACCCCAATGCCAAAGGCAAGGACTGGCAGATGTTA 2475
Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2476 GCACAGAAAAACAGCATCAACAGGAATTTATCTTATTCGCTACACAAGTAGCCCATCT 2535
Qy 41 AlaMetIleLeuAsnLeuTTPGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2536 GCTGTCATTTGAACCTTGGAGAGATTGGGAGGACATCATCAGCATGATGGTGATCTTGGACTCCCTG 2595
Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
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Db 2596 GCCTGTGCCCTTGAAGAGATTGGGAGGACACACACGAACTCTCAAACATTTCAGAATCC 2655
Qy 81 Glu 81
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Db 2656 CAG 2658

Search completed: September 9, 2005, 09:52:08
Job time : 144.111 secs

GenCore version 5.1.6
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OW protein - nucleic search, using frame_plus_p2n model

Run on: September 9, 2005, 04:41:16 ; Search time 808.309 Seconds
(without alignments)
658.098 Million cell updates/sec

Title: US-10-624-932C-2_COPY_817_897
Perfect score: 423
Sequence: 1 QKISSLDPPCRGADWRTL.....AAVAGLQDPDAGLFTVSEAE 81

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	423	100.0	2752	18	US-10-624-932-1	Sequence 1, Appli
3	423	100.0	2881	10	US-09-970-944-1	Sequence 1, Appli
4	423	100.0	3561	20	US-10-643-795A-77	Sequence 77, Appl
5	423	100.0	3561	21	US-10-948-518-77	Sequence 77, Appl
6	423	100.0	3580	17	US-10-311-623-13	Sequence 13, Appl
7	410	96.9	2697	16	US-10-240-154-15	Sequence 15, Appl
8	410	96.9	3014	10	US-09-933-261-1	Sequence 1, Appli
9	410	96.9	3014	14	US-10-256-702-1	Sequence 1, Appli
10	393	92.9	1269	14	US-10-103-313-36	Sequence 36, Appl
11	376	88.9	1787	10	US-09-933-261-2	Sequence 2, Appli
12	376	88.9	1787	14	US-10-256-702-2	Sequence 2, Appli
13	368	87.0	1321	18	US-10-296-115-365	Sequence 365, App
14	364	86.1	574	9	US-09-764-861-20	Sequence 20, Appl
15	364	86.1	574	10	US-09-764-861-20	Sequence 20, Appl
16	364	86.1	574	14	US-10-103-313-192	Sequence 192, App
17	364	86.1	574	14	US-10-115-328-20	Sequence 20, Appl
c 18	357.5	84.5	9582	9	US-09-764-861-62	Sequence 62, Appl
c 19	357.5	84.5	9582	10	US-09-764-861-62	Sequence 62, Appl
c 20	357.5	84.5	9582	14	US-10-115-928-62	Sequence 62, Appl
c 21	351.5	83.1	18772	9	US-09-764-861-63	Sequence 63, Appl
c 22	351.5	83.1	18772	10	US-09-764-861-63	Sequence 63, Appl
c 23	351.5	83.1	18772	14	US-10-115-328-63	Sequence 63, Appl
c 24	327	77.3	600	22	US-10-972-079-78338	Sequence 78338, A
c 25	327	77.3	600	22	US-10-972-079-78339	Sequence 78339, A
c 26	304	71.9	341	9	US-09-867-701-3673	Sequence 3673, Ap
c 27	234	55.3	599	22	US-10-972-079-78337	Sequence 78337, A
c 28	201	47.5	3866	21	US-10-764-420-2213	Sequence 2213, Ap
c 29	198	46.8	2831	10	US-09-933-261-3	Sequence 3, Appli
c 30	198	46.8	2831	14	US-10-256-702-3	Sequence 3, Appli
c 31	191	45.2	2406	17	US-10-108-260A-239	Sequence 239, App
c 32	191	45.2	2860	17	US-10-087-684-1	Sequence 1, Appli
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c 36	191	45.2	2895	18	US-10-037-417-37	Sequence 37, Appl
c 37	191	45.2	2995	11	US-09-972-211-55	Sequence 55, Appl
c 38	191	45.2	2995	18	US-10-096-625-55	Sequence 55, Appl
c 39	191	45.2	3485	9	US-09-816-828-18	Sequence 18, Appl
c 40	191	45.2	3501	17	US-10-295-027-1123	Sequence 1123, Ap
c 41	191	45.2	3884	14	US-10-028-072-145	Sequence 145, App
c 42	191	45.2	3884	14	US-10-140-808-145	Sequence 145, App
c 43	191	45.2	3884	14	US-10-121-049-145	Sequence 145, App
c 44	191	45.2	3884	14	US-10-123-904-145	Sequence 145, App
c 45	191	45.2	3884	14	US-10-140-470-145	Sequence 145, App

ALIGNMENTS

RESULT 1
US-09-918-779-1
; Sequence 1, Application US/09918779
; Publication No. US20030064369A1
; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shmukets, Richard
; APPLICANT: Zethusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William

```
; APPLICANT: Alsbrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/09/918,779
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: 2001-07-30
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,697
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/263,662
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/281,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-779-1

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Score: 423.00 Matches: 81
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

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Qy 61 AlaAlaAlaValAlaGlyLeuGlyGlnProAspAlaGlyLeuPheThrValSerGluAla 80
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Qy 81 Glu 81
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; GENERAL INFORMATION:
; APPLICANT: Taupier, Raymond
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Rastelli, Luca
; APPLICANT: Spaderna, Steven
; APPLICANT: Shimkets, Richard
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Spytek, Kimberly
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Gusev, Vladimir
; APPLICANT: Grosse, William
; APPLICANT: Alsbrook, John
; APPLICANT: Lepley, Denise
; APPLICANT: Burgess, Catherine
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Stone, David
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-074 US
; CURRENT APPLICATION NUMBER: US/10/624,932
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/918,779
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/221,409
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/222,840
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,752
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,762
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,770
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/223,769
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: 60/225,146
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,392
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 60/225,470
; PRIOR FILING DATE: 2000-08-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-624-932-1
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Score: 423.00 Matches: 81
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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; Publication No. US20030204052A1
; GENERAL INFORMATION:
; APPLICANT: Herrman, John L
; APPLICANT: Rastelli, Luca
; APPLICANT: Shinkets, Richard A
; TITLE OF INVENTION: No. US20030204052A1el Proteins and Nucleic Acids Encoding Same an
; FILE REFERENCE: 21402-138
; CURRENT APPLICATION NUMBER: US/09/970,944
; PRIOR FILING DATE: 2002-05-02
; PRIOR FILING DATE: 2000-10-04
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; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2881
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-970-944-1

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; Sequence 77, Application US/10643795A
; Publication No. US20040241703A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/643,795A
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-643-795A-77

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Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0

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Qy 21 AlaGlnLysLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
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Db 2404 GCCATGATCTCTCAACTGTGGAGGCGGGCACTTCCCAACGGCAACTCAGCCAGCTG 2463
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Qy 81 Glu 81
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; Sequence 77, Application US/10948518
; Publication No. US20050064492A1
; GENERAL INFORMATION:
; APPLICANT: FREDERIC J. DESAUVAGE
; APPLICANT: GRETCHEN FRANTZ
; APPLICANT: KENNETH J. HILLAN
; APPLICANT: PAUL POLAKIS
; APPLICANT: ANDREW POLSON
```

```
; APPLICANT: VICTORIA SMITH
; APPLICANT: SUSAN D. SPENCER
; APPLICANT: THOMAS D. WU
; APPLICANT: ZEMIN ZHANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF TUMOR
; FILE REFERENCE: P5026R1-US
; CURRENT APPLICATION NUMBER: US/10/948,518
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: US/10/643,795
; PRIOR FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 77
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-948-518-77

Alignment Scores:
Pred. No.: 5.5e-49 Length: 3561
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

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Db 2284 CAGAAGATAATTTCCAGCTGGACCCACCTGTAGGCGGGTGGCGGACTCTG 2343
Qy 21 AlaGlnlyLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2344 GCCAGAAATCCACCTGGACAGCATCTCAGCTTCTTTGCTCCAAAGCCAGCCCCACA 2403
Qy 41 AlaMetlleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2404 GCCATGATCTCTACCTGTGGAGGGCGGCGGACTTCCCAAGCGGACCTCAGCGAGCTG 2463
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2464 GCTGCAGCAGTGGCTGGAGTGGCGAGCCAGCAGCTGGCCCTCTTCACAGTGTGCGAGGCT 2523
Qy 81 Glu 81
Db 2524 GAG 2526

RESULT 6
US-10-311-623-13
; Sequence 13, Application US/10311623
; Publication No. US20040023244A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; GRIFFIN, Jennifer A.
; APPLICANT: KALLICK, Deborah A.; TRIBOULEY, Catherine M.
; APPLICANT: YUE, Henry; NGUYEN, Daniel B.
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.
; APPLICANT: POLICKY, Jennifer L.; AZIMZAI, Yalda
; APPLICANT: LU, Dnyung Aina M.; GRAUL, Richard C.
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
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; APPLICANT: BANDMAN, Olga; ARVIZU, Chandra S.
; APPLICANT: YANG, Junming; XU, Yuming
; APPLICANT: GANDHI, Ameena R.; WARREN, Bridget A.
; APPLICANT: DING, Li; SANJANWALA, Madhusudan M.
; APPLICANT: DUGGAN, Brendan M.; LU, Yan
; TITLE OF INVENTION: RECEPTORS
; FILE REFERENCE: PF-0793 USN
; CURRENT APPLICATION NUMBER: US/10/311,623
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 01/19942
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/214,027
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: US 60/228,045
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/255,104
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 3580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023244A1 6052371CB1
US-10-311-623-13

Alignment Scores:
Pred. No.: 5.54e-49 Length: 3580
Score: 423.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-10-624-932c-2_COPY_817_897 (1-81) x US-10-311-623-13 (1-3580)
Qy 1 GlnlysllelleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2284 CAGAAGATAATTTCCAGCTGGACCCACCTGTAGGCGGGTGGCGGACTCTG 2343
Qy 21 AlaGlnlyLeuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2344 GCCAGAAATCCACCTGGACAGCATCTCAGCTTCTTTGCTCCAAAGCCAGCCCCACA 2403
Qy 41 AlaMetlleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2404 GCCATGATCTCTACCTGTGGAGGGCGGCGGACTTCCCAAGCGGACCTCAGCGAGCTG 2463
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2464 GCTGCAGCAGTGGCTGGAGTGGCGGCGGAGCCAGCAGCTGGCCCTCTTCACAGTGTGCGAGGCT 2523
Qy 81 Glu 81
Db 2524 GAG 2526

RESULT 7
US-10-240-154-15
; Sequence 15, Application US/10240154
; Publication No. US20030175741A1
; GENERAL INFORMATION:
; APPLICANT: Cochran et al.
; TITLE OF INVENTION: SCHIZOPHRENIA RELATED GENES
; FILE REFERENCE: CRFW-P01-006
; CURRENT APPLICATION NUMBER: US/10/240,154
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: PCT/GB01/01486
; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
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; LENGTH: 2697
; TYPE: DNA
; ORGANISM: Rattus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2697)
US-10-240-154-15

Alignment Scores:
Pred. No.: 2,7e-47 Length: 2697
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservativeness: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
DB: 16 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-10-240-154-15 (1-2697)
Qy 1 GlnYsIlleIleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2449 CAAAGATCATCGCCAGTCTGGACCCACCTGCAGCGGGCGCGACTGGAGAACTCTA 2508
Qy 21 AlaGlnYsLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
Db 2509 GCCCAGAAATTCACCTGGACAGCCATCTTAGCTTTCTTGCCCTCCAAAGCCGAGCCCTACA 2568
Qy 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2569 GCCATGATCTCAACCTATGGAGGACGACGACCTTCCCAACGGCAACTCGGCCAGCTG 2628
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2629 GCAGCAGCTGTGGCGGAGTGGCCAAACAGATGCTGCGCTCTTTCACGGTGTGGAGGCC 2688
Qy 81 Glu 81
Db 2689 GAG 2691

RESULT 8
US-09-933-261-1
; Sequence 1, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-933-261-1

Alignment Scores:
Pred. No.: 3.11e-47 Length: 3014
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservativeness: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
DB: 10 Gaps: 0

US-10-624-932C-2_COPY_817_897 (1-81) x US-09-933-261-1 (1-3014)
Qy 1 GlnYsIlleIleSerSerLeuAspProProCysArgArgGlyAlaAspTrpArgThrLeu 20
Db 2449 CAAAGATCATCGCCAGTCTGGACCCACCTGCAGCGGGCGCGACTGGAGAACTCTA 2508
Qy 21 AlaGlnYsLeuHisLeuAspSerHisLeuSerPheAlaSerLysProSerProThr 40
Db 2509 GCCCAGAAATTCACCTGGACAGCCATCTTAGCTTTCTTGCCCTCCAAAGCCGAGCCCTACA 2568
Qy 41 AlaMetIleLeuAsnLeuTrpGluAlaArgHisPheProAsnGlyAsnLeuSerGlnLeu 60
Db 2569 GCCATGATCTCAACCTATGGAGGACGACGACCTTCCCAACGGCAACTCGGCCAGCTG 2628
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2629 GCAGCAGCTGTGGCGGAGTGGCCAAACAGATGCTGCGCTCTTTCACGGTGTGGAGGCC 2688
Qy 81 Glu 81
Db 2689 GAG 2691

RESULT 9
US-10-256-702-1
; Sequence 1, Application US/10256702
; Publication No. US20030059859A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsay
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/256,702
; FILING DATE: 27-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
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; FILING DATE: 20-Aug-2001
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-256-702-1
Alignment Scores:
Pred. No.: 3,11e-47 Length: 3014
Score: 410.00 Matches: 78
Percent Similarity: 97.53% Conservative: 1
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 96.93% Indels: 0
DB: 14 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x US-10-256-702-1 (1-3014)
Qy 1 GlnlyvlelleSerSerLeuAspProProCysArgArgGlyAlaAspTtpArgThrLeu 20
Db 2449 CAAAGATCATCGCGAGTGTGAGCCACCTTGCAGCGGGCGCGAGTGGAGAACTCTA 2508
Qy 21 AlaGlnlyvleuHisLeuAspSerHisLeuSerPhePheAlaSerLysProSerProThr 40
Db 2509 GCCCAGAAACTTCACTTGGACAGCCATCTTAGCTTCTTTGGCTCCAAGCCAGCCCTACA 2568
Qy 41 AlaMetilleuAenLeuTtpGluAlaArgHisPheProAenglyAenLeuSerGlnleu 60
Db 2569 GCCATGATCTCTCAACCTATGGAGGCGACGGCACCTTCCCAACGGCAACCTCGGCCAGCTG 2628
Qy 61 AlaAlaAlaValAlaGlyLeuGlnProAspAlaGlyLeuPheThrValSerGluAla 80
Db 2629 GCACGAGCTGTGGCGGAGTGGGCGAACACCATGCTGGCCCTTTCACGGTGTGGAGGCC 2688
Qy 81 Glu 81
Db 2689 GAG 2691
RESULT 10
US-10-103-313-36
; Sequence 36, Application US/10103313
; Publication No. US20030082758A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-103-313-36
Alignment Scores:
Pred. No.: 2.69e-45 Length: 1269
Score: 393.00 Matches: 74
Percent Similarity: 100.00% Conservative: 0
; FILING DATE: 20-Aug-2001
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1787 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-933-261-2
Alignment Scores:
Pred. No.: 1.07e-42 Length: 1787
Score: 376.00 Matches: 77
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.91% Indels: 0
DB: 14 Gaps: 0
US-10-624-932C-2_COPY_817_897 (1-81) x US-10-103-313-36 (1-1269)
Qy 8 AspProProCysArgArgGlyAlaAspTtpArgThrLeuAlaGlnlyvleuHisLeuAsp 27
Db 9 GACCCACCCTGTAGCGGGGTGGCGACTGGCGGACTTGGCCCAAGAACTCCACCTGGAC 68
Qy 28 SerHisLeuSerPhePheAlaSerLysProSerProThrAlaMetilleuAenLeuTtp 47
Db 69 AGCCATCTCAGCTTCTTTGGCTTCAAGCCAGCCAGCCCATGATCCTCAACCTGTGG 128
Qy 48 GluAlaArgHisPheProAenglyAenLeuSerGlnleuAlaAlaValAlaGlyLeu 67
Db 129 GAGCGCGGCACTTCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGAGCTG 188
Qy 68 GlyGlnProAspAlaGlyLeuPheThrValSerGluAlaGlu 81
Db 189 GCCCAGCCAGCGCTGGCCCTTTCACAGTGTGGAGGCTGAG 230
RESULT 11
US-09-933-261-2
; Sequence 2, Application US/09933261
; Publication No. US20030040046A1
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; Leonardo, E. David
; Hink, Lindsey
; Masu, Masayuki
; Kazuko, Keino-Masu
; TITLE OF INVENTION: Netrin Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 BUSH STREET, SUITE 3200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/933,261
; FILING DATE: 20-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/808,982
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC96-217
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1787 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-933-261-2
Alignment Scores:
Pred. No.: 1.07e-42 Length: 1787
Score: 376.00 Matches: 77
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